

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 175861

TO: Jeanine Goldberg

Location: rem/2D15/2C70

Art Unit: 1634

Tuesday, January 10, 2006

Case Serial Number: 09/954586

From: Barb O'Bryen

Location: Biotech-Chem Library

Remsen 1a69

Phone: 571-272-2518

POS

barbara.obryen@uspto.gov

Search Notes

RUSH



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STIC-Biotech/ChemLib

175861 Mg

"∕From:

Chan, Christina

Sent:

Friday, January 06, 2006 1:23 PM

To:

Subject:

Goldberg, Jeanine; Fredman, Jeffrey; STIC-Biotech/ChemLib

RE: ALLOWANCE AF Search for 09/954586

Please mush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

----Original Message-----

From:

Goldberg, Jeanine

Sent: To: Friday, January 06, 2006 11:44 AM Chan, Christina; Fredman, Jeffrey

Subject:

ALLOWANCE AF Search for 09/954586

Please search SEQ ID NO: 46 and 59.

THANK YOU! Jeanine

Jeanine Anne Goldberg 1634 571-272-0743

REM 2D15 Mailbox: 2C70

Searcher Phone:

Date completed:

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Compositions, methods and kits for determining the presence cryptosporidium organisms in a test sample
Patent: WO 0222890-A 33 21-MAR-2002;
Gen-Probe Incorporated (US)
Location/Qualifiers
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Compositions, methods and kits for determining the presence cryptosporidium organisms in a test sample
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Gen-Probe Incorporated (US)
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Compositions, methods and kits for determining the presence cryptosporidium organisms in a test sample
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Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRNi genes from field-collected roots
Grassl. Sci. 47, 1-8 (2001)
2 (bases 1 to 143)
3 2 (bases 1 to 143)
5 Saito, K.
Direct Submission
5 Submitted (04-AUG-2000) Katsuharu Saito, National Institute of Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno, Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp, Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp, Tel:81-287-37-7691, Fax:81-287-36-6629)
Location/Qualifiers
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Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRN
genes from field-collected roots
Grassl. Sci. 47, 1-8 (2001)

2 (bases 1 to 144)

Saito, K.

Direct Submission

Loubmitted (04-AUG-2000) Katsuharu Saito, National Institute of
Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno,
Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp,
Tel:81-287-37-7691, Fax:81-287-36-6629)
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endophyte DG vagiga2
Eukaryota; Fungi; Ascomycota; environmental
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Pred. No.
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endophyte DG vagiga5
endophyte DG vagiga5
Eukaryota; Fungi; Ascomycota;
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Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRN
genes from field-collected roots
Grassl. Sci. 47, 1-8 (2001)
2 (bases 1 to 144)
3 Saito, K.

Direct Submission
Submitted (04-AUG-2000) Katsuharu Saito, National Institute of
Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno,
Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp,
Tochigi, 329-2791, Fax:81-287-36-6629)
Location/Qualifiers
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Endophyte DG vagiga3 gene for small subunit ribosomal RN
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Endophyte DG vagiga4 gene for small subunit ribosomal RN
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2 (bases 1 to 144)
Saito, K.
Direct Submission
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Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;
Glomeraceae; Glomus.
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Submitted (04-AUG-2000) Katsuharu Saito, National Institute of Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno, Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp, Tel:81-287-37-7691, Fax:81-287-36-6629)
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Number J01353"
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Scutellospora sp. Scut1
Scutellospora sp. Scut1
Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Diversisporales;
Gigasporaceae; Scutellospora.

Gigasporaceae; Scutellospora.

Gigasporaceae; Scutellospora.

Clapp, J.P., Young, J.W., Merryweather, J.W. and Fitter, A.H.

Diversity of fungal symbionts in arbuscular mycorrhizas from a natural community

L New Phytol. 130 (2), 259-265 (1995)

E 2 (bases 1 to 145)
S Clapp, J.P.

Direct Submission

Loanied (18-APR-1995) Justin P. Clapp, Biology, University of york, Heslington, York, North Yorkshire YOI 5YW, England

Location/Qualifiers
                                                                                     Scutellospora sp. Scut2

Scutellospora sp. Scut2

Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Diversisporales; Gigasporaceae; Scutellospora.

Gigasporaceae; Scutellospora.

I (bases 1 to 145)

S Clapp, J.P., Young, J.W., Merryweather, J.W. and Fitter, A.H.

Diversity of fungal symbionts in arbuscular mycorrhizas from a natural community

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S Clapp, J.P.

Clapp, J.P.

Direct Submission

L Submitted (18-APR-1995) Justin P. Clapp, Biology, University of Submitted (18-APR-1995) Justin York, North Yorkshire YOl 5YW, England

Location/Qualifiers
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RNA gene of Saccharomyces cerevisiae, GenBank
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ORIGIN

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Best Local Similarity 100.0%;
Matches 23; Conservative 0

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Scoring table

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geneseqn2003cs: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES	
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Result	1)t		Query				
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U	N	23	00		9	AAD38438	Aad38438 Cryptospo
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ALIGNMENTS

dB dB Hybridisation; amplification; detection; target DNA #8 вр 2000US-0232028P 11-SEP-2001; 2001WO-US042192 AAD38426 standard; DNA; 23 entry) (first Cryptosporidium sp. Cryptosporidium sp WO200222890-A2 12-SEP-2000; 10-SEP-2002 21-MAR-2002 AAD38426 RESULT 1

Weisburg WG; PD, (GENP-) GEN-PROBE INC Stull Cunningham MM,

Novel oligonucleotides functioning as hybridization probes, helper probes and/or primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms, useful for detecting the organism in a test WPI; 2002-454395/48. sample

Claim 23; Page 8; 133pp; English

The invention relates to oligonucleotides functioning as hybridisation assay probes, helper probes and/or amplification primers, targetted to nucleic acid sequences derived from Cryptosporidium organisms. Probes and primers of the invention are useful for detecting the presence of Cryptosporidium organisms in general and C. parvum organisms in particular in a test sample. The present sequence is Cryptosporidium app. target DNA

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This invention relates to a novel method for monitoring differential expression of genes in a filamentous fungal cell. Specifically, it refers to identifying differential gene expression occurring between two related filamentous fungal cells to a substrate array of nucleic acids of filamentous fungal cells to a substrate array of ruchoderma reesei (T. reesei) expressed sequenced tags (ESTs), or suppression subtractive hybridization (SSH) clones and detecting a signal in the array. The present invention further describes a computer readable medium having for monitoring differential expression of several genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells. It also provides a search unit for comparing a target sequence to a T. reesei EST sequence of the data storage unit to identify homologous sequences, and a retrieval unit for obtaining the homologous sequence(s). Accordingly, it provides a microorganism is grown on cellulose or corn stover, as well as for
                                                                                                                                                                                                                       ö
                                                                  and
                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monitoring differential expression of genes of two filamentous fungal cells, for e.g. discovering new genes, comprises adding labeled nucleic acids to an array of Trichoderma reesei expressed sequenced tags and
                              The invention relates to oligonucleotides functioning as hybridisation assay probes, helper probes and/or amplification primers, targetted to nucleic acid sequences derived from Cryptosporidium organisms. Probes primers of the invention are useful for detecting the presence of Cryptosporidium organisms in general and C. parvum organisms in particular in a test sample. The present sequence is C. parvum target I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                        Gaps
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  Page
                                                                                                                                                       32 BP;
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discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Note that this method utilizes an array where one spot equals one gene or open reading frame, which makes extensive follow-up characterization unnecessary since sequence information is available and EST and/or SSH microarrays can be organized based on function of the gene products. This polynucleotide sequence is a T. reesei SSH cDNA clone that forms part of the substrate array of the invention. NOTE: The SeqIDs 1-1188 referring to T. reesei ESTs or SSH clones or their combinations are available in electronic form from the USPTO web site
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                                                                                                ID:200500699
                                                                                                                                      Length 384;
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                                                                                                                   Sequence 384 BP; 108 A; 83 C; 88 G; 105 T; 0 U;
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No. 0.23;
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Mismatches
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Pred. No. (
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endomycorrhizal
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                                                                                                                            Query Match
Best Local Similarity
23; Conserv
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                                                                                                                             Nuclear 18S ribosomal gene; SSU; probe; primer; arbuscular endomycorrhizal fungi; plant; root;
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Pred. No. 0.23;
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standard; DNA; 447
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endomycorrhizal fungi in pl
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Best Local Similarity
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design taxon specific primers/probes
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 C; 107 G; 117 T;
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containing dinoflagellates in seas, lakes,
ponds and pools.
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The invention relates to a method for selecting an anti-microbial agent, comprising: (A) the microbial analysis step of analysing the microbial phase of a sample based on DNA base sequences (e.g. by PCR); and (B) the continuation of a sample based on DNA base sequences (e.g. by PCR); and (B) the continuation of a sample based on DNA base sequences (e.g. by PCR); and (B) the continuation of a sample based to choose anti-microbial agents for treatment of microorganism-containing samples, to monitor the effect of added antimicrobial agent over time in a sample or process, to inhibit or regulate slime in paper manufacturing and for the analysis of adherent or products during manufacture, in which DNAs are extracted from the paper products during manufacture, in which bnAs are extracted from the adherent-causing microorganisms for analysis to reveal the microbial phase or predominant or specific microorganism, e.g. slime, after comparison. The method is used for screening and selecting anti-microbial and selecting anti-microbial phase or product adherenteling and treating slimes in papermaking industry, which can also be applied in monitoring anti-microbial effect, analysis of product adherents. The present sequence is a Filamentous control or the invention control or the method of the invention control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New method, useful in screening anti-microbial agents for controlling slimes in papermaking industry or monitoring anti-microbial effect, comprises microbial analysis step and anti-microbial selection step.
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                                         PCR; primer;
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Filamentous fungi 18S rDNA partial
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10-JUL-2001; 2001JP-00209845
29-NOV-2001; 2001JP-00365004
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                                         Antimicrobial agent; slime;
18S rDNA; filamentous fungi.
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ALIGNMENTS

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DEFINITION	AU012137 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc06398, mRNA seguence.
ACCESSION	AU012137
VERSION	AU012137.1 GI:3357046
DS	BST.
SOURCE	
ORGANISM	charomyces pombe
	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
	י במי
REFERENCE	1 (bases 1 to 154)
AUTHORS	Mita, K.
TITLE	Identification of expressed sequence tags of Schizosaccharomyces
	pombe
JOURNAL	
COMMENT	Contact: Mitsuoki Morimyo
	esearch Group
	nstitute of Radiological Sciences
	9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
	Email: morimyo@nirs.go.jp.
FEATURES	Location/Qualifiers
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	/clone_lib="Schizosaccharomyces pombe late_log phase CDNA"
	/note="Vector: M13mp19; The cDNA library of
	Schizosaccharomyces pombe are available for searching on
	the World Wide Web. (URL, nctp://www.nirs.go.jp/"
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/sex="h minus"
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/clone lib="Schizosaccharomyces pombe was prepared by cloning cDNA
/note="Vector: M13mp19; The cDNA library of
/note="vector: M13mp19; The cDNA library of
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schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
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Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
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/university"
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Schizosaccharomyces pombe (fission yeast)
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1 (bases 1 to 193)

Morimyo, M. and Mita, K.

Identification of expressed sequence tags of
                                                                                                                                                                                            organism="Lycopersicon esculentum"
'mol_type="mRNA"
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Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 191)
van der Hoeven, R.S., Bezzerides, J.l., Matern, A.L., Holt, I.E.,
Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S.,
Ronning, C.M., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and
Tanksley, S.D.
Generation of ESTs from tomato flower tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4896"
/db_xref="taxon:4896"
/clone="spc06817"
/sex="h minus"
/clone lib="Schizosaccharomyces pombe late log phase cDN?
/note="Vector: M13mp19; The cDNA library of
/note="Vector: M13mp19; The cDNA library of
into the SmaI site of M13mp19 DNA and the direction of DN
sequences was not always from 5' to 3'. The cDNA data of
sequences was not always from 5' to 3'. The cDNA data of
schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
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AU012452 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc06817, mRNA sequence
AU012452.1 GI:3357361
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EST296603 tomato flower buds, anthesis, Cornell University Lycopersicon esculentum cDNA clone cTODIC1 similar to Ipome hederacea 18S ribosomal RNA gene, mRNA sequence.
AW217889
AW217889.1 GI:6528763
EST.
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Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555,
Email: morimyo@nirs.go.jp.
                                                                                                                                                                                                                                     Schizosaccharomyces pombe (fission yeast)
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 154)
Morimyo, M. and Mita, K.
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/mol_type="mRNA"
/strain="972"
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ACCESSION VERSION

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ORGANISM

REFERENCE AUTHORS TITLE

COMMENT

FEATURES

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/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
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/sex="h minus"
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/clone_lib="Schizosaccharomyces pombe was prepared by cloning cDNA
/note="Vector: M13mp19; The cDNA library of
/note="vector: M13mp19; The cDNA library of
schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of M13mp19 DNA and the direction of DNA
into the Smal site of M13mp19 DNA and the direction of Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
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/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/clone_lib="AS"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library
was made from the aerial part (above the collar) of 6
was made from the aerial part (above the bollar) of 6
three weeks old seedlings grown in hydroponic conditions. A
three weeks drought stress treatment was applied by
lowering the osmotic potential of the nutrient solution
                    Schizosaccharomyces
                                 pombe
Unpublished (1998)
Contact: Mitsuoki Morimyo
Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Jag
Bmail: morimyo@nirs.go.jp.
Email: morimyo@nirs.go.jp.
Location/Qualifiers
- 108
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Pinus pinaster
Pinus pinaster
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Coniferopaida; Coniferales; Pinaceae; Pin
1 (bases 1 to 216)
Frigerio, J. and Plomion, C.
Identification of water-deficit responsive genes in Mari
(Pinus pinaster Ait.) using an EST approach
Unpublished (2002)
Contact: Frigerio JM
Genetique et Amelioration 69
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Email: Frigerio@pierroton.inra.fr
Seg primer: T3.
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/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="AS01F05"
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Morimyo, M. and Mita, K
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/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
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/sex="h minus"
/clone lib="Schizosaccharomyces pombe was prepared by cloning cDNA
/note="Vector: M13mp19; The cDNA library of
/note="Vector: M13mp19; The cDNA library of
into the Smal site of M13mp19 DNA and the direction of DNA
into the Smal site of M13mp19 DNA and the direction of Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
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AU009944 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc00704, mRNA sequence
AU009944.1 GI:3346624
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Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555,
Email: morimyo@nirs.go.jp.
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AU010607 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc10128, mRNA se
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Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetae;
                          Length 193;
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1 (bases 1 to 200)

Morimyo, M. and Mita, K.

Identification of expressed sequence tags of
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                           Score 23;
Pred. No.
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Unpublished (1998)
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Tracheophyta; Pinua; Pinua.

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DEFINITION

RESULT 6 AU010607

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VERSION KEYWORDS SOURCE

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BACKWARD: Universal M13 reverse primer Plate: 30 row: C column: 7
Seq primer: M13 reverse primer High quality sequence stop: 229
POLYA=No.
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Pred. No. 0.64;
; Mismatches
                                                                                                                     Contact: El-Dorry, Hamza
Department of Biochemistry
Institute of Chemistry. University of
Avenida Professor Lineu Prestes, 748,
BRASIL
                                                                                                                                                                                                                                                FORWARD: Universal M13 forward primer
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illarity 100.0%; I
Conservative 0;
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                                                                                                                                                                                              Tel: (55) 11-38183848
Fax: (55) 11-38183848
Email: dorry@iq.usp.br
PCR PRimers
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Trest-A2885
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CF945596
CF945596.1
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Best Local
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CF945596
                             REFERENCE
AUTHORS
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PUBMED
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Tr-A2815 5', mRNA
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. hordei
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. mRNA sequence
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-0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"
                                                                                                                                                                                                                                                              CDNA CLINA 20051

AW791051.1

GI:13902648

EST.

Blumeria graminis f. sp. hordei

SM Blumeria graminis f. sp. hordei

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;

Erysiphales; Erysiphaceae; Blumeria.

CE 1 (bases 1 to 222)

RS Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver, R.P.

'Aentification in the fungal pathogen Blumeria graminis b
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                                                                                                                      Gaps
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Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
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                                                                                           Length 216;
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                                                                                                                                                                                                                                     AW791051
D00369-R Lambda Zap, Stratagene Blumeria graminis
CDNA clone D00369 similar to hypothetical protein
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clone 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="conidia"
/lab_host="Hordeum vulgare"
/clone_lib="Lambda Zap, Stratagene"
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rea jecorina cDNA
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No. 0.64;
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                                                                                         Score 23; DB 1;
Pred. No. 0.64;
; Mismatches
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/organism="Blumeria graminis
/mol_type="mRNA"
/db_xref="taxon:62688"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 Gl. Carlsbergvej, DK-2500,
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: swr@crc.dk
High quality sequence stop: 2:
POLYA=No.
                                                                                                                                             Score
Pred.
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Hypocrea jecorina
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233 bp mRNA linear EST 19-NOV-2003 TrEST-A Hypocrea jecorina cDNA clone Tr-A2885 5', mRNA
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Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 233)
Chambergo, F.S., Bonaccorsi, E.D., Ferreira, A.J.S., Ramos, A.S.P.,
Ferreira, J.R.Jr., Abrahao-Neto, J., Farah, J.P.S. and El-Dorry, H.
Elucidation of the metabolic fate of glucose in the filamentous
fungus Trichoderma reesei using expressed sequence tag (EST)
analysis and cDNA microarrays
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

(hambergo, F.S., Bonaccorsi, E.D., Ferreira, A.J.S., Ramos, A.S.P., Ferreira, J.R.Jr., Abrahao-Neto, J., Farah, J.P.S. and El-Dorry, H. Elucidation of the metabolic fate of glucose in the filamentous fungus Trichoderma reesei using expressed sequence tag (EST) analysis and cDNA microarrays
J. Biol. Chem. 277 (16), 13983-13988 (2002)
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(55) 11-38183848
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Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

I (bases 1 to 236)
S Chambergo, F.S., Bonaccorsi, E.D., Ferreira, A.J.S., Ramos, A.S.P.,
Ferreira, J.R.Jr., Abrahao-Neto, J., Farah, J.P.S. and El-Dorry, H.
Elucidation of the metabolic fate of glucose in the filamentous fungus Trichoderma reesei using expressed sequence tag (EST)
analysis and cDNA microarrays
J. Biol. Chem. 277 (16), 13983-13988 (2002)
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clone Tr-A2
                                                                        SP,
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Department of Biochemistry
Institute of Chemistry. University of Sao Paulo
Avenida Professor Lineu Prestes, 748, Sao Paulo,
                                                           Sao Paulo
Sao Paulo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 bp mRNA
Trest-A Hypocrea jecorina cDNA
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                                                                                                                                                            FORWARD: Universal M13 forward primer BACKWARD: Universal M13 reverse primer Plate: 31 row: A column: 5
                                                                                                                                                                                                                                                                      /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM9414 (ATCC26921)"
/db_xref="taxon:51453"
                               Contact: El-Dorry, Hamza
Department of Biochemistry
Institute of Chemistry. University of
Avenida Professor Lineu Prestes, 748,
     (16), 13983-13988
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Seq primer: M13 reverse primer
High quality sequence stop: 232
POLYA=No.
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                                                                                                                                                                                                                                                                                                                                                 sex="Asexual"
                                                                                                   Tel: (55) 11-38183848
Fax: (55) 11-38183848
Email: dorry@iq.usp.br
PCR PRimers
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    Chem. 277
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23; Conserv
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CF945185
CF945185.1
EST.
     J. Biol.
11825887
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CF945185
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Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' (the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA532319
CpEST.449 unizAPCpIOWAsporoLib3 Cryptosporidium parvum cDNA 5', AA532319.1 GI:2276511
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                                                                                                                                                                                                                                                                                                                                    7;
Email: dorry@iq.usp.br
PCR PRimers
FORWARD: Universal M13 forward primer
BACKWARD: Universal M13 reverse primer
Plate: 30 row: G column: 7
Seq primer: M13 reverse primer
High quality sequence stop: 230
POLYA=No.
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Sed primer: M13 reverse
High quality sequence stop: 254
Location/Qualifiers
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Conservative
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/dev_stage="sporozoite"
/lab_host="E. coli XL1 Blue MRF' Kan"
/lab_host="E. coli XL1 Blue MRF' Kan"
/clone_lib="uniZAPCPIOWAsporoLib3"
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/note="Vector: UniZAP XR; Site_1: EcoR I; Site_2: Xho I;
The C. parvum cDNA library was prepared by Drs. Norman J. Pieniazek, Michael J. Arrowood, Susan B. Slemenda, and Jan R. Mead at the Centers for Disease Control and Prevention (Atlanta, Georgia). Poly A+ RNA was separated from total C. parvum RNA using the Poly(A) Quik mRNA Isolation Kit from Stratagene. Directional cDNA was synthesized by first-strand priming with a Xho I-oligo d(T)
linker-primer, second-stranding with RNase H and DNA polymerase I, ligation of EcoR I linkers, and digestion with Xho I, all using the Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned into the EcoR I and Xho I sites of Lambda Uni-ZAP XR vector; the unamplified library was >95% recombinant and contained a X 10(6) independent
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                                                                                                                                                                                                                                                                                                                                                                                                                                     cated that
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Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

1 (bases 1 to 256)
Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,
Bhatterai, K. and Dean, R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                           clones. PCR analysis of 20 random clones indicated that the average insert size was ca. 1.1 kb."
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mgmk014xB02f.b pmkl in pBluescriptII sk(-) plasmid Magnagrisea cDNA clone mgmk014xB02 5', mRNA sequence.
CD029939.1 GI:30411775
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Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see c person; Best nr hit (April. 22, 2003) ref | XP 284680.1 | hypothetical protein 2 (rRNA externa. . . 31 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Length 254;
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Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 7
organism="Cryptosporidium parvum"
|mol_type="mRNA"
|strain="IOWA"
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100.0%; Pred. No. 0.65;
ttive 0; Mismatches
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Plate: mgmk014 row:
Seq primer: T3.
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Tel: 979
Fax: 979
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CD029939
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/sex="mat1-1 hermaphrodite"
/sex="Mat1-1 hermaphrodite"
/cell_type="germinated conidia"
/clone_lib="pmk1 in pBluescriptII sk(-) plasmid"
/clone_lib="pmk1 in pBluescriptII sk(-) plasmid"
/note="Vector: pBluescriptSK; Site_1: EcoRI; Site_2: XhoI;
Conidia germinated in hydrophobic surface membrane in 27C
for 12 hours. NN95 is a hygromycin phosphotransferase gene
replacement of the PMK1 MAP kinase gene in the Guy11
strain background (Xu and Hamer. 1996. Genes & Dev.
10:2696). Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,

Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.

Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.

1 (bases 1 to 269)

S Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P.L.,

Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueyes, E.,

Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K.,

Miller, R., Ortega, J., Pavlova, I., Perea, J., Todisco, S.,

Trujillo, R., Valentine, J., Wells, A., Werner-Washburne, M., Yazzie, S.,

and Natvig, D.O.

Expressed sequences from conidial, mycelial, and sexual stages of

Neurospora crassa

Fungal Genet. Biol. 21, 348-363 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI398053
NCSC2C4T7 Subtracted Conidial Neurospora crassa cDNA clone SC2C4
3', mRNA sequence.
AI398053.
AI398053.1 GI:4241138
EST.
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/dev_stage="Germinating conidia"
/lab_host="E. coli"
/clone_lib="Subtracted Conidial"
/note="Vector: pBlueScript SK (-); Site_l: EcoRI; Site_2:
XhoI; mRNA isolated from germinating conidia, grown in lx
Vogel's, 2% sucrose for 4.5 hours. cDNA directionally
cloned into pBluescript SK(-) using the Uni-ZAP XR vector
system (Stratagene, La Jolla, CA). Previously identified
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Department of Biology
University of New Mexico
Castetter Hall, Albuquerque, NM 87131,
Tel: 505 277 3411
Fax: 505 277 0304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 6, 100.0%; Pred. No. 0.65; ive 0; Mismatches
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/mol_type="mRNA"
/strain="74-OR23-IV A (FGSC 2/db_xref="taxon:5141"
/clone="SC2C4"
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Location/Qualifiers
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BACKWARD: T7 primer
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Plate: mgcw009 row: E column: 23
Seq primer: T3.

Location/Qualifiers
L. 278

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/ clone=lib="RCW Lambda Zap"
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mgcw005xE23f.b RCW Lambda Zap Express Library Magnaporthe grisea cDNA clone mgcw009xE23 5', mRNA sequence.

BU638475.1 GI:23350801

EST.
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Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person; Best nr hit (April. 22, 2003) gb|EAA21331.1| hypothetical
protein [Plasmodium yoelii yoelii] 35 0.21
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Magnaporthe grisea
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

1 (bases 1 to 278)
Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,
Bhatterai, K. and Dean, R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthegrisea
Unpublished (2002)
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highly expressed clones were subtracted from library."
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Length 278;

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21:16:55 9, 2006, Search completed: January Job time: 2480 secs

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/cgn2_6/ptodata/1/ina/1_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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US-08-093-144-6
US-08-093-144-4
US-08-093-144-4
US-09-533-559-3436
US-09-533-559-3436
US-08-949-770-1
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US-09-533-559-3436
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US-09-281-766-1
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US-09-533-559-4068
US-09-957-995A-1
US-09-957-995A-1
US-09-998-416-178
US-08-998-416-281
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5.1.6
Compugen
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ALIGNMENTS

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US-08-093-144-5
Sequence 5, Application US/08093144
Patent No. 5434048
GENERAL INFORMATION:
APPLICANT: BIMON, LUC
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF TITLE OF INVENTION: DNA PROBES CUSHMAN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Bleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTY: Washington
STATE: DOS STATE: Tape
COMPUTER READABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
COUNTY: APPLICATION DATA:
APPLICATION NUMBER: US/08/093,144
FILING DATE:
CLASSIFICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hymo, Lawrence A.
REGISTRATION NUMBER: 19,057
REFERENCE/OCKET NUMBER: 19,057
RELEPRA: (5102) 861-3000
TELEFONE: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDUSS: Gouble
TOPOLOGY: linear
US-08-093-144-5
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Length

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US-09-533-559-1021/c

Sequence 1021, Application US/09533559

Fatent No. 6902887

GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Apfirey R.Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: D Groth Clausen
APPLICANT: D Groth Clausen
APPLICANT: Beter Bjarke Olsen
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
TITLE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT APPLICATION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1021
LENGTH: 570
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                                                                                                                                                                      APPLICATION NUMBER: US/08/093,144
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               'A:
US/08/093,144
                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
Eleventh Floor, 1615
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nucleic acid
EDNESS: double
                            STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
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; LOCATION: (1)...(570)
; OTHER INFORMATION: n =
US-09-533-559-1021
                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patent1
              Washington
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TOPOLOGY: linear
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Pred. No. (
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hymo, Lawrence A.
                                                                                                                                                                                                                                                                                          CUSHMAN
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Patent No. 5434048;
GENERAL INFORMATION:
APPLICANT: SIMON, LUC
APPLICANT: LALONDE, MAURICE
TITLE OF INVENTION: DNA PROBES FOR
                                                                                                                        US-08-093-144-6
; Sequence 6, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FO
; TITLE OF INVENTION: ARBUSCULAR EN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/093,1
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APPLICANT: LALONDE, MAURICE
TITLE OF INVENTION: DNA PROBES FOR TITLE OF INVENTION: ARBUSCULAR EN NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUN
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REFERENCE/DOCKET NUMBER: LAH/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEO ID NO
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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   Conservative
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC (OPERATING SYSTEM: SOFTWARE: PatentIr
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Matches 23; Conser
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US-08-093-144-4
; Sequence 4, Ap
 23;
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STATE:
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1788 base pairs
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DATA:
                    CLASSIFICATION: 43:
PRIOR APPLICATION DATA
APPLICATION NUMBER:
FILING DATE:
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Matches 23
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Patent No. 6063604
GENERAL INFORMATION:
APPLICANT: Wick, James F.
APPLICANT: Mueller, Reinhold
APPLICANT: Blassak, Michele
APPLICANT: Wilkosz, Richard K.
TITLE OF INVENTION: Target Nucleic Acid Sequence Amplificati
                         0
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                                                                                                                                                                                                      APPLICANT: Randy M. Berka
APPLICANT: Randy M. Rey
APPLICANT: Aichael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
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South Wacker Drive
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Pred. No. 0.096;
Mismatches
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                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147
                                                                           422 GGATAACCGTGGTAATTCTAGAG 400
           Pred
                                                                                                                                                             3436, Application US/0953355
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         Similarity 100.0%; 123; Conservative 0;
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6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(617)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Fusarium venenatum
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CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                               Patent No. 6902887
GENERAL INFORMATION:
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US-09-533-559-3436
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SEQ ID NO 3436
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-08-949-770-1
            Local
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Suite 800
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                                                                                                                                                                                                                                                                                                                                                of
                                ATTORNEY/AGENT INFORMATION:
NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 28003/33045
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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parvum"
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MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08867820A Patent No. 5891685 GENERAL INFORMATION:
08/617,045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: YAMAGISHI Masahiro
APPLICANT: TAKAI Yukie
APPLICANT: MIKAWA Takashi
APPLICANT: HARA Mari
APPLICANT: HARA Mari
APPLICANT: OHARA Akiko
TITLE OF INVENTION: METHOD FOR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 1416
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Similarity 100.0%;
23; Conservative 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: June 3, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                               : 1750 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                         hame/KEY: misc feature corner in other information: /= corner information: par us-08-949-770-1
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                                   th 100.0%;
Similarity 100.0%;
23; Conservative 0;
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US-09-645-073-1
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Similarity 95.7%;
22; Conservative
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23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        Q ID NO 1
LENGTH: 2293
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-09-645-073-1
          US-10-121-740-1
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                                      Query Match
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                                                                                                                                    Length 1788
                                                                                                                                                                                                                                                                                                                               APPLICANT: Strobel, Gary
APPLICANT: Manker, Denise
TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
TITLE OF INVENTION: USE
FILE REFERENCE: AQ 2019.40
CURRENT APPLICATION NUMBER: US/10/121,740
CURRENT APPLICATION NUMBER: 60/283,902
PRIOR APPLICATION NUMBER: 60/283,902
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10121740
; Patent No. 6911338
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
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Patent No. 6911338
GENERAL INFORMATION:
APPLICANT: Strobel, Gary
APPLICANT: Manker, Denise
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Candida albical
                                                                              Candida albicans
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|larity 100.0%;
|Conservative (
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23; Conservative
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ORGANISM: Muscodor albus
                                                                                            MUCL29800
                                                                                                                                                   Similarity
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SOFTWARE: Fast:
SEQ ID NO 1
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2055
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                                                                                                                                                              23;
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                                                                                             STRAIN:
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Matches
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                                                                                                                                                              Matches
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Length 2089
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US-09-396-196G-761

Sequence 761, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 761

LENGTH: 25
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Pred. No. 0.11;
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                0.11;
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Pred. No. 0.45;
0; Mismatches
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  DB
Score 23; DB Pred. No. 0.1; Mismatches
                                                                                                                                                                             Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; TITLE OF INVENTION:
; FILE REFERENCE: L02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT APPLICATION NUMBER: US 60/151,770
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin version 3.0
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PRIOR APPLICATION NUMBER: JP
PRIOR FILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
y Match
Local Similarity 95.7%;
hes 22; Conservative
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Job time: 105.5 Becs
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Best Local Similarity
Matches 22; Conser
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US-09-815-981A-5
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US-09-270-767-10466
; Sequence 10466, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila mel;
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila mel;
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 10466
; LENGTH: 312
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/720,587A
FILING DATE: 19910628
CLASSIFICATION: 435
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NUCLEIC ACIDS PROBES
TO HISTOPLASMA CAPSULATUM
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0; Mismatches
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described
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IR: 193/121
         RESULT 12
US-07-720-587A-2/c
; Sequence 2, Application US/07720587A
; Patent No. 5352579
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                                                                                                                                                                                             Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 193/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
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Best Local Similarity 95.7%;
Matches 22; Conservative
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1 West Sixth
                                                                      GENERAL INFORMATION:
APPLICANT: Curt L. Milli
TITLE OF INVENTION: NUCI
TITLE OF INVENTION: TO F
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-7
TELEFAX: (213) 955-04
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ZIP: 90017
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US-09-805-127-7
Sequence 7, Application US/09805127
Fatent No. 6653119
GENERAL INFORMATION:
TITLE OF INVENTION: WHITE ROT FUNGI AND METHOD FOR DECOMPOSING DIOXINS USING
TITLE OF INVENTION: WHOTE
FILE REFERENCE: WKO-101PCT
CURRENT APPLICATION NUMBER: US/09/805,127
CURRENT FILING DATE: 2001-03-14
CURRENT FILING DATE: 2001-03-14
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Score 21.4; DB 3;
Pred. No. 0.55;
0; Mismatches 1.
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Pred. No. 0.76
0; Mismatches
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APPLICANT: de Jong, Gary
APPLICANT: Vandebyl, Sandra
TITLE OF INVENTION: MCLECULES INTO CELLS AND FILE REFERENCE: 24601-4168; CURRENT APPLICATION NUMBER: US/09/815,981A; CURRENT FILING DATE: 2001-03-22; NUMBER OF SEQ ID NOS: 13; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                   1 GGATAACCGTGGTAATTCTAGAG
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Local Similarity 95.7%;
les 22; Conservative
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Compugen Ltd
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Post-processing: Minimum Match 0%

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Listing first 45 summaries

Database: Published Applications NA Main:*

1: /cgn2 6/ptodata/1/pubpna/US07_PUBCOMB.

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Minimum Maximum published Applications NA_Main:*

1: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appli	Appl	Appl	A.	6, Ap	, App
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	US-09-954-695-46	-954-695-	-09-954-695-5	-09-954-695-6	-4	US-09-954-586-52	US-09-954-586-58	-954-586-	-2	-09-954-69	US-09-954-695-37	-09-954-69	US-09-954-586-29	0	US-09-954-586-37	9	US-10-950-009-47	US-10-466-016-6	US-10-950-009-48	US-10-950-009-49	US-10-653-047-1021	US-10-653-047-3436	US-10-094-097B-112
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9 US-10-483-439-1	6 US-10-121-740-3	7 US-10-623-432-3	10 US-11-131-659-3	6 US-10-121-740-1		10 US-11-131-659-1	8 US-10-719-900-602235	9 US-10-809-189-761	8 US-10-357-930-12550	8 US-10-357-930-14189	US-10-3	6 US-10-264-049-1193	US-10-3	8 US-10-357-930-33712	8 US-10-357-930-12578	_	6 US-10-125-968-281	_	US-09-92	•	10 US-11-060-867-93
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ALIGNMENTS

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Sequence 46, Application US/09954695

| Sequence 46, Application US/09954695
| Patent No. US20020055116A1
| GENERAL INFORMATION:
| APPLICANT: CUNNINGHAM, Melissa M. APPLICANT: STULL, Paul D. APPLICANT: WEISBURG, William G. APPLICANT: WEISBURG, William G. APPLICANT: WEISBURG, William G. APPLICANT: WEISBURG, William G. APPLICANT: WEISBURG, WILL G. INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
| TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
| FILE REFERENCE: GP116-02.UT
| CURRENT PILING DATE: 2001-09-11
| CURRENT PILING DATE: 2001-09-12
| NUMBER OF SEO ID NOS: 69
| SEO ID NOS: 69
| SEO ID NO 46
| LENGTH: 23
| TYPE: DNA
| ORGANISM: Artificial Sequence
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US-09-954-695-52
US-09-954-695-52
; Sequence 52, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE; FILE REFERENCE: GP116-02.UT; CURRENT APPLICATION NUMBER: US/09/954,695
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No. 0.18;
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US-09-954-695-46
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ORGANISM: Artificial Sequence
FEATURE:
                                             Seguence
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                                                                        Synthetic
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                         46, Application U
5. US20020146717A1
            LENGTH: 23
TYPE: RNA
ORGANISM: Artificial
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                                                                                                                                   Similarity
23; Conserv
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CTHER INFORMATION:
US-09-954-695-64
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US-09-954-586-46
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US-09-954-586-52
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Patent No.
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; Sequence 58, Application US/09954695
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-09-12
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APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
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Pred. No. 0.18;
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CURRENT APPLICATION NUMBER: US/09/954,695
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/232,028
PRIOR FILING DATE: 2000-09-12
             60/232,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic Construct US-09-954-695-58
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llarity 73.9%;
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SOFTWARE: PatentIn version 3.1
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SOFTWARE: PatentIn version 3.1
            PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-09-12 NUMBER OF SEQ ID NOS: 69 SOFTWARE: Patentin version 3.
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ORGANISM: Artificial
                                                                                                                     ORGANISM: Artificial FEATURE:
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Best Local Similarity
Matches 17; Conser
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Best Local Similarity
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 FILING DATE:
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LENGTH: 23
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LENGTH: 23
                                                                                                         TYPE: RNA
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GENERAL INFORMATION:

APPLICANT: CUNNINGHAM, Melissa M.

APPLICANT: STULL, Paul D.

APPLICANT: WEISBURG, William G.

TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DE

TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN

FILE REFERENCE: GP116-03.UT

CURRENT APPLICATION NUMBER: US/09/954,586

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/232,028

PRIOR FILING DATE: 2000-09-12

NUMBER OF SEQ ID NOS: 69

SOFTWARE: Patentin version 3.1

SEQ ID NO 46

LENGTH: 23
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Patent No. US20020146717A1

GENERAL INFORMATION:
APPLICANT: CUNNINGHAM, Melissa M.
APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AN TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM FILE REFERENCE: GP116-03.UT
CURRENT APPLICATION NUMBER: US/09/954,586
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52
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APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE FILE REFERENCE: GP116-02.UT CURRENT APPLICATION NUMBER: US/09/954,695
CURRENT FILLING DATE: 2001-09-11
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US-09-954-695-33
; Sequence 33, Application US/09954695
; Patent No. US20020055116A1
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: STULL, Paul D.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-09-12
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Pred. No. 0.19;
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Pred. No. 0.19;
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PRIOR FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.1
SEQ ID NO 29
LENGTH: 32
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Patent No. US20020055116A1
GENERAL INFORMATION:
APPLICANT: CUNNINGHAM, Melissa M.
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larity 73.9%;
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin version 3.1
SEQ ID NO 33
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Synthetic
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APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE FILE REFERENCE: GP116-03.UT CURRENT APPLICATION NUMBER: US/09/954,586 CURRENT FILING DATE: 2001-09-11 PRIOR APPLICATION NUMBER: US 60/232,028 PRIOR FILING DATE: 2000-09-12
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APPLICANT: STULL, Paul D.
APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE FILE REFERENCE: GP116-03.UT
CURRENT APPLICATION NUMBER: US/09/954,586
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/232,028
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.1
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Patent No. US20020146717A1
GENERAL INFORMATION:
APPLICANT: CUNNINGHAM, Melissa M.
APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
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ORGANISM: Artificial Sequence
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larity 73.9%;
Conservative (
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; Sequence 64, Application US,
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Meli
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Best Local Similarity
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9-954-586-64
 ; OTHER INFORMATION:
US-09-954-586-52
                                                                                                                                                                                                         RESULT 7
US-09-954-586-58/C
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APPLICANT: STULL, Paul D.
APPLICANT: STULL, Paul D.
APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
FILE REFERENCE: GP116-03.UT
CURRENT APPLICATION NUMBER: US/09/954,586
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/232,028
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.1
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; Sequence 33, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AN
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
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STULL, Paul D.
WEISBURG, William G.
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ORGANISM: Artificial Sequence
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                                   CUNNINGHAM,
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US-09-954-586-33
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US-09-954-586-29
Patent No. USZOUZUL4
GENERAL INFORMATION:
APPLICANT: CUNNINGH
APPLICANT: STULL,
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LENGTH: 32
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US-09-954-695-41/c
US-09-954-695-41/c
; Sequence 41, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INCRMATION:
; APPLICANT: CUNNINGHAM, Melissa M.;
; APPLICANT: STULL, Paul D.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: COMPOSITIONS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2001-09-12
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Version 3.1
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APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINI
TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
FILE REFERENCE: GP116-02.UT
CURRENT APPLICATION NUMBER: US/09/954,695
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/232,028
PRIOR FILING DATE: 2000-09-12
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US-09-954-586-29
; Sequence 29, Application US/09954586
                                                                     Sequence 37, Application US/09954695
Patent No. US20020055116A1
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SOFTWARE: PatentIn version 3.1
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TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-37
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US-11-136-527-8154

US-10-750-623-40363

US-11-136-527-8154

US-11-136-527-8154

US-10-750-623-40363

US-11-136-527-8154

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US-11-750-623-203

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US-11-136-527-4032
; Sequence 4032, Application US/11136527
; Publication No. US20050287570A1
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Express
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-26
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4032
; LENGTH: 1874
; TYPE: DNA
; ORGANISM: Rattus norvegicus
ALIGNMENTS
                                                                            Sequence 1, Application US/10519379;
Publication No. US20050255126A1;
GENERAL INFORMATION:
APPLICANT: ASAHI DENKA Co., Ltd.
TITLE OF INVENTION: Microorganism and FILLE OF INVENTION: Microorganism;
FILE REFERENCE: A0301;
CURRENT APPLICATION NUMBER: US/10/519,379;
CURRENT FILING DATE: 2004-12-27
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US-11-136-527-174864

Sequence 174864, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth

APPLICANT: Wyeth

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 174864

LENGTH: 1920
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TITLE OF INVENTION: Probe Arrays For Expression Profiling
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
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SOFTWARE: Patentin version 3.2
LENGTH: 1920
TYPE: PATERIAN SECTION 3.2
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; Sequence 174865, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
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US-11-136-527-174865
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US-11-136-527-174866
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US-11-136-527-4032
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i Sequence 210, Application US/10775169

j Sequence 210, Application US/10775169

j Publication No. US20050287532A9

j GENERAL INFORMATION:

j APPLICANT: Wyeth

j APPLICANT: Twine, Natalie

j APPLICANT: Twine, Natalie

j APPLICANT: Trepicchio, William

j APPLICANT: Trepicchio, William

j TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo

j TITLE OF INVENTION NUMBER: US/10/775,169

CURRENT FILING DATE: 2004-02-11

j NUMBER OF SEQ ID NOS: 5278

j SOFTWARE: PatentIn version 3.2

j SEQ ID NO 210

LENGTH: 1969
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Mismatches
Sequence 174866, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

TITLE OF INVENTION: Probe Arrays For Express

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

SEQ ID NO 174866

LENGTH: 1920
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LOCATION: (57)...(61)
OTHER INFORMATION: Each "n" represents a 1
OTHER INFORMATION: contains no nucleotide
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US-10-947-249-33
; Sequence 33, Application US/10947249
; Publication No. US20050287541A1
; GENERAL INFORMATION:
; APPLICANT: Akira NAKAGAWARA
; APPLICANT: Miki OHIRA
; APPLICANT: Shin ISHII
. APPLICANT: Takeshi GOTO
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Pred.
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ilarity 95.7%;
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                                                                                                                                                                                                                                                                                                 norvegicus
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ORGANISM: Homo sapiens
FEATURE:
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or

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RESULT 10
US-10-750-623-31917/C
; Sequence 31917, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MAI GENOMICS, INC.
; APPLICANT: KERR, Richard
; APPLICANT: KOSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
APPLICANT: Deblac,
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
LENGTH: 1391
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Pred. No. 29;
0; Mismatches
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 31917
LENGTH: 1391
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Christophe FG
Philip M
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; Sequence 205, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    880 GGATAACTGTGGTAATTTGAAAG
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MMI GENOMICS, INC.
DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
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Best Local Similarity
Matches 19; Conser
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hes 19; Conser
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US-11-117-187-187

Sequence 187, Application US/11117187

Publication No. US20050266560A1

GENERAL INFORMATION:

APPLICANT: PREUSS, DAPHNE

APPLICANT: COPENHAVER, GREGORY

ITILE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND ME

FILE REFERENCE: ARCD:309US;
CURRENT APPLICATION NUMBER: US/11/117,187

CURRENT FILING DATE: 2005-04-28

PRIOR APPLICATION NUMBER: 60/125,219

PRIOR FILING DATE: 1999-03-18

NUMBER OF SEQ ID NOS: 212

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 187

LENGTH: 59590
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                                                                         the Prognosis of of Neuroblastoma
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                                     APPLICANT: Yasuko YOSHIDA
APPLICANT: Saichi YAMADA
TITLE OF INVENTION: Microarray for Predicting
TITLE OF INVENTION: Predicting the Prognosis
FILE REFERENCE: 117007
                                                                                                                        CURRENT APPLICATION NUMBER: US/10/947,249
CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US 60/505,614
PRIOR APPLICATION NUMBER: 2003-09-25
NUMBER OF SEQ ID NOS: 200
SOFTWARE: Patentin version 3.1
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US-10-750-185-31917/c
; Sequence 31917, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
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nilarity 95.7%;
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                         HIRATA
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LOCATION: (2521)..(57768)
OTHER INFORMATION: N = A,
      Hiroyuki KUBO
Takahiro HIRA
                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature;
LOCATION: (57)...(61);
OTHER INFORMATION: n is
US-10-947-249-33
                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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hes 22; Conser
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nes 22; Conser
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                                                                                                                                                                                                                                    SEQ ID NO 33
LENGTH: 1969
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Best Local S
Matches 22
        APPLICANT:
APPLICANT:
APPLICANT:
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ilarity 94.4%;
Conservative
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Best Local Similarity
Matches 17; Conser
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                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-30025
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CRGANISM: Bovine
US-10-750-623-30025
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Matches 17
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Pred. No. 29;
0; Mismatches
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Pred. No. 29;
0; Mismatches
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US-10-873-528-245

Sequence 245, Application US/10873528

Publication No. US20050276814A1

GENERAL INFORMATION:

APPLICANT: Microbial Technics Limited

APPLICANT: Hansbro, Philip M

TITLE OF INVENTION: Proteins

FILE REFERENCE: PWC/P21129WO

CURRENT APPLICATION NUMBER: US/10/873,528

CURRENT FILING DATE: 2004-06-23

PRIOR FILING DATE: 2001-01-26

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 388

SOFTWARE: PatentIN Ver: 2.1

SEQ ID NO 245

LENGTH: 1542
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/10/873,528
CURRENT FILING DATE: 2004-06-23
PRIOR APPLICATION NUMBER: US/09/769,787
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 388
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                                                                                                                                                                                                                                              ; ORGANISM: Streptococcus pneumoniae US-10-873-528-205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Streptococcus pneumoniae US-10-873-528-245
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APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
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Similarity 82.6%;
19; Conservative
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Similarity 82.6%;
19; Conservative
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SEQ ID NO 205
LENGTH: 1542
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Best Local S
Matches 19
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Best Local S
Matches 19
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APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRA:
FILE REFERENCE: MMILLOO-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 30025
LENGTH: 3688
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                       TRAITS
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRA
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 30025
LENGTH: 3688
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APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
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Pred. No. 44;
0; Mismatches
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Mismatches
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Pred. No. 4
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; Sequence 30025, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: RERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; ROFTWARE: PROPILE 2002-11-14
; SOFTWARE: Proprietary
; CONGANISM: Homo sapiens
; LENGANISM: Homo sapiens
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
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Best Local Similarity 89:5%; Pred. No. 34;

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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.

1 (bases 1 to 413)
Nagano, Y., Finn, M.B., Lowery, C.J., Murphy, T., McCorry, K.A., Crothers, E., Watabe, M., Rao, J.R., Dooley, J.S.G., Rooney, P.J. Matsuda, M. and Moore, J.E.
Cryptosporidium parvum 18S rRNA partial gene sequence
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Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 415)
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Submitted (18-DEC-2003) Department of Bacteric Ireland Public Health Laboratory, Belfast City Road, Belfast, Co. Antrim BT9 7AD, Northern Incoation/Qualifiers

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    organism="Cryptosporidium parvum"
'mol_type="genomic DNA"
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Cryptosporidiidae; Cryptosporidium.

1 (bases 1 to 660)
Morgan, U.M., Monis, P.T., Xiao, L., Limor, J., Sulaiman, I., Raido O'Donoghue, P., Gasser, R., Murray, A., Fayer, R., Blagburn, B.L., Lal, A.A. and Thompson, A.R.C.
Molecular and phylogenetic characterisation of Cryptosporidium
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Direct Submission
Submitted (26-OCT-2000) Division of Veterinary and Biomedical
Science, Murdoch University, Murdoch Drive, Perth, WA 6150,
Australia
                                                                                                                         646 bp DNA linear INV 02-8
parvum strain bovine 18S ribosomal RNA gene,
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Evaluation of Cryptosporidium oocysts and Giardia watershed reservoir
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/organism="Cryptosporidium parvum"
/mol_type="genomic DNA"
/strain="bovine"
/db_xref="taxon:5807"
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18S ribosomal RNA
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Direct Submission
Submitted (11-APR-2005) EPA/ORD/NRMRL,
Dr., Ada, OK 74820, USA
Location/Qualifiers
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/product="18S ribosomal RNA"
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Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa;
Cryptosporidiidae; Cryptosporidium.
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Pred. No.
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AF262332.1 GI:11761742
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c and
                                                                 Finn, M.B., Lowery, C.J., Nagano, Y., Moore, J.E. and Dooley, J.S.G. Direct Submission
Submitted (18-DEC-2003) Department of Bacteriology, Northern Ireland Public Health Laboratory, Belfast City Hospital, Lisburn Road, Belfast, Co. Antrim BT9 7AD, Northern Ireland, UK
Location/Qualifiers
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      Rooney, P.J
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Submitted (02-MAY-2000) Division of Parasitic Diseases, Consease Control and Prevention, 4770 Buford Highway, F-12, Chamblee, GA 30341, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cryptosporidium sp.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida Cryptosporidiidae; Cryptosporidium.

L (bases 1 to 600)
Xiao, L., Alderisio, K., Limor, J., Royer, M. and Lal, A.A. Identification of species and sources of Cryptosporidi storm waters with a small-subunit rRNA-based diagnosti genotyping tool
Appl. Environ. Microbiol. 66 (12), 5492-5498 (2000)
                                                                                                                                                                                                                                         a fox"
Crothers, E., Watabe, M., Rao, J.R., Dooley, J.S.G., Room
Matsuda, M. and Moore, J.E.
Cryptosporidium parvum 18S rRNA partial gene sequence
Unpublished
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/mol_type="genomic DNA"
/strain="Fox8"
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/country="USA: New York"
/note="isolated from storm waters
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Pred. No. 7.2;
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|mol_type="genomic DNA"
|isolate="N"
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'db_xref="taxon:5807"
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Cryptosporidium sp. Q1
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 665)
Morgan, U.M., Monis, P.T., Xiao, L., Limor, J., Sulaiman, I., Raidal, O'Donoghue, P., Gasser, R., Murray, A., Fayer, R., Blagburn, B.L., Lal, A.A. and Thompson, A.R.C.
Molecular and phylogenetic characterisation of Cryptosporidium findian
                                                                                                                                                                                                                                                                sequence.
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Cryptosporidium parvum 18S ribosomal RNA gene, partial
AF162429
AF162429.1 GI:5916184
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                                                                                                                  Length 660;
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Morgan, U.M., Monis, P.T. and Xiao, L.
Direct Submission
Submitted (26-OCT-2000) Division of Veterinary and Science, Murdoch University, Murdoch Drive, Perth, Australia
            BD1
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/mol type="genomic DNA"
/isolate="Q1"
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        /organism="Cryptosporidium/mol_type="genomic_DNA"/isolate="BD1"
                                                                                                                             red. No. 7;
Mismatches
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Mismatches
                                        /specific_host="black duck
/db_xref="taxon:150840"
                                                                                                                   Score 23;
Pred. No.
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Pred. No.
                                                                      <1. . . > 660
/product = "18S ribosomal
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/db_xref="taxon:150841"
<1. .>665
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nilarity 100.0%;
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linear INV 18-JUN-2005 small subunit ribosomal RNA
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Multi-locus genotyping of Cryptosporidium species from HIV-infected
individuals with and without diarrhea in southern India
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                                                                                       Grandis, S.A.,
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Cryptosporidiidae; Cryptosporidium.

I (bases 1 to 704)

Blears, M.J., Pokorny, N.J., Carreno, R.A., Chen, S., De Grandis, S.P. Lee, H. and Trevors, J.T.

DNA fingerprinting of Cryptosporidium parvum isolates using amplified fragment length polymorphism (AFLP)

J. Parasitol. 86 (4), 838-841 (2000)

10958466

2 (bases 1 to 704)

Bokorny, N.J.

Direct Submission

Submitted (24-JUN-1999) Environmental Biology, University of Guelph, Edmund C. Bovey Building, Guelph, ON NIG 2W1, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        College
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coccidia, Eimeriida
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/mol_type="genomic DNA"
/strain="HLA"
/db_xref="taxon:5807"
/country="USA: Louisiana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Cryptosporidium parvum"
|mol_type="genomic DNA"
|strain="vlr200443"
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<1. .>712
/product="small subunit ribosomal
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DQ067569
DQ067569.1 GI:67527112
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Pred. No. 6.9;
); Mismatches
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Pred. No. 6.9;
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Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa;
Cryptosporidiidae; Cryptosporidium.
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Location/Qualifiers
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23; Conserv
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Xiao, L.
30341,
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Matches 23
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                                                                                                                                                                    Cryptosporidium sp.

Cryptosporidium sp.

Eukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;

Cryptosporidiidae; Cryptosporidium.

E 1 (bases 1 to 715)

S Xiao, L., Alderisio, K., Limor, J., Royer, M. and Lal, A.A.

Identification of species and sources of Cryptosporidium oocysts in storm waters with a small-subunit rRNA-based diagnostic and genotyping tool

L Appl. Environ. Microbiol. 66 (12), 5492-5498 (2000)

L Appl. Environ. Microbiol. 66 (12), 5492-5498 (2000)

L Appl. Environ. Microbiol. 66 (12), Super, M. and Lal, A.A.

E 2 (bases 1 to 715)

S Xiao, L., Alderisio, K., Limor, J.R., Royer, M. and Lal, A.A.

Direct Submission

L Submitted (02-MAY-2000) Division of Parasitic Diseases, Centers for Disease Control and Prevention, 4770 Buford Highway, F-12,

Chamblee, GA 30341, USA

Location/Qualifiers
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AY268582
AY268582.1 GI:33347884
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Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 744)
                                                                DNA linear INV small subunit ribosomal l
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Junge,R., Sulaiman,I.M., Zhou,L., Arrowood,M.J., Koude
Modry,D. and Lal,A.A.
Genetic diversity of Cryptosporidium spp. in captive 1
Appl. Environ. Microbiol. 70 (2), 891-899 (2004)
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product="small subunit ribosomal RNA"
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note="isolated from storm waters
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red. No. 6.9;
Mismatches 0
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Direct Submission
Submitted (07-APR-2003) CDC, DPD/NCID,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Cryptosporidium s
/mol_type="genomic DNA"
/isolate="KK"
/db_xref="taxon:90962"
/country="USA: New York"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23;
Pred. No.
                                                                715 bp
sp. isolate KK
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<1. .>715
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                                                                                                                                                            Cryptosporidium sp
                                                                              Cryptosporidium sp
partial sequence.
AF262326
AF262326.1 GI:117
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                                    RESULT 13
AF262326/c
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Genetic diversity of Cryptosporidium app. in captive reptiles Appl. Environ. Microbiol. 70 (2), 891-899 (2004)
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/organism="Cryptosporidium parvum"
/mol type="genomic DNA"
/isolate="1444, mouse genotype"
/specific_host="Elaphe guttata guttata"
/db_xref="taxon:5807"
<1. .>748
/product="small subunit ribosomal RNA"
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                                                                                                                                                                          Length
1. .744
/organism="Cryptosporidium parvum"
/mol type="genomic DNA"
/isolate="1432, bovine genotype"
/specific_host="Iguana iguana"
/db_xref="taxon:5807"
<1. .>744
                                                                                                                       ribosomal
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Pred. No. 6.8;
; Mismatches
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larity 100.0%; Pred. No. 6.8;
Conservative 0; Mismatches
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Cryptosporidium parvum
Eukaryota, Alveolata, Apicomplexa,
Cryptosporidiidae, Cryptosporidium.
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/product="small subunit
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AY268583
AY268583.1 GI:33347885
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Submitted (07-APR-2003) CDC,
30341, USA
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; Search time 327 Seconds (without alignments) 468.770 Million cell updates/sec
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23 ccgtaaagttattatgagtcacc US-09-954-586-59 23 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

residues 4996997 seqs, 3332346308 Searched: 9993994 of hits satisfying chosen parameters: Total number

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printed, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.

		Description	3427	Aad38439 Cryptospo	45	33		16368 Nucle	71867 G. vesi	7	71868 G. intr	56146	45 Aspergi	586 Asperg	589	e 9	57	0 Asper	0030 Xylar	1286 Bulg	Adp79725 Anti-tumo
SUMMARIES		QI	AAD38427	AAD38439	AAD38445	AAD38433	AAT90818	AAA46368	AAQ71867	~		4	AAF11545	ADU55586		AAF11316	ADU55357	AD293360	ABZ80030	AA168286	ADP79725
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ALIGNMENTS

ф Hybridisation; amplification; detection; target DNA #9 вр 2001WO-US042192 2000US-0232028P 23 entry) RESULT 1 AAD38427/c ID AAD38427 Btandard; DNA; (GENP-) GEN-PROBE INC (first Cryptosporidium sp. Cryptosporidium sp WO200222890-A2 11-SEP-2001; 12-SEP-2000; 10-SEP-2002 21-MAR-2002 AAD38427

Weisburg WG; Ω, Stull WPI; 2002-454395/48. Cunningham MM,

Novel oligonucleotides functioning as hybridization probes, helper probes and/or primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms, useful for detecting the organism in a test sample.

Claim 23; Page 8; 133pp; English

The invention relates to oligonucleotides functioning as hybridisation assay probes, helper probes and/or amplification primers, targetted to nucleic acid sequences derived from Cryptosporidium organisms. Probes and primers of the invention are useful for detecting the presence of Cryptosporidium organisms in general and C. parvum organisms in particular in a test sample. The present sequence is Cryptosporidium sp. target DNA

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The invention relates to oligonucleotides functioning as hybridisation assay probes, targetted to nucleic acid sequences derived from Cryptosporidium organisms. Probes primers of the invention are useful for detecting the presence of Cryptosporidium organisms in general and C. parvum organisms in particular in a test sample. The present sequence is Cryptosporidium sparticular in a test sample.
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and/or primers, targeted to nucleic acid sequences derived from
Cryptosporidium organisms, useful for detecting the organism in
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of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
            forensic analysis, environmental resting and studies involving developmental and cellular biology. The methods are versatile, reliable and simple and are capable of amplifying both RNA and DNA, and should do so exponentially, using a minimum number of primers under substantially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes an isothermal target nucleic acid amplification method. The method comprises contacting a mixture of a target, two primers containing hemi-modified restriction endonuclease sites and modified nucleotides capable of forming phosphodiester bonds, and a polymerase lacking 5' to 3' exonuclease activity, with a restriction endonuclease, and incubating under isothermal conditions. I method can be used for amplifying nucleotide sequences. The method exhibits improved thermodynamics and kinetics, resulting in increased sensitivity and polynucleotide length, thus broadening both the range target sources and the range of target lengths. The present sequence represents the 18S ribosomal DNA of C. parvum, and contains a RNA targe (nucleotides 937-1095) which is used to demonstrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid, with improved
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of metabolism,
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endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
intraradices and Gigaspora margarita were compared with that of a
arbuscular endomycorrhizal fungus, Endogone pisiformis, in order
design taxon specific primers/probes
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larity 90.9%; Pred. No. 57;
Conservative 0; Mismatches
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Abe K;
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                                                                                                                                                                                                                                                                                                              SEQ ID NO
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                                                                                                       d. No. 57;
Mismatches
                                                                                       Score 18.8;
Pred. No. 57;
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                                                               C; 107
                                                                                                                                                                                                                                                                                                                                      fermentation;
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fermentation and growth
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Kobayashi
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Takeuchi M,
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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTS provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF11248 to AAF11247 represents ESTS from Aspergillus niger; AAF11854 to AAF14878 represents ESTS from Aspergillus niger; AAF11854 to AAF14878 represents ESTS from Aspergillus are all specifically claimed in the present
                                                                                                                                                                                                                                                     expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering;
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ed. No. 58;
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Pred.
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CGTTAAGTTATTATGAATCACC
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                                                                                                                                                                                                                                                                                                                                                                                  WO200056762-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2000;
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AAF11545
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81.7%; 90.9%;

Query Match Best Local Similarity

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The invention relates to a method for monitoring the differential expression of genes in a first filamentous fungal cell relative to the same genes in one or more second filamentous fungal cells. The method involves differentially labeling nucleic acids from the first and second fungal cells with fluorescent reporter dyes, and adding the mixture of fungal cells with fluorescent reporter dyes, and adding the mixture of fluorescently labeled polynucleotides to a substrate containing an array of Fusarium venenatum expressed sequence tags (ESTS) selected from ADUS1519-ADUS5288 under conditions that permit hybridization. Relative expression of genes in the fungal cells is determined by fluorescence; the fluorescent signal emitted when labeled nucleic acids from the first fungal cell bind to the ESTS in the array differs in color from that emitted when labeled nucleic acids bind to the array, a distinct combined fluorescence emission color is produced. The filamentous fungal cells used in the method are chosen from Acremonium, Aspergillus, Fusarium Thielavia, Tolypocladium, and Trichoderma cells, preferably Fusarium venenatum, Aspergillus niger, or Aspergillus oryzae. The method of the invention is useful for monitoring the expression of a plurality of genes in filamentous fungal cells, in order to improve the cells, in order to improve the cinterest.
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relative to expression of the genes in second filamentous fungal
comprises using microarrays containing Fusarium venenatum express
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG,
                                                                                                                                                                                                                                                   microarray; hybridization; EST;
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     228
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249 CGTTAAGTTATTATGATTCACC
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22-MAR-2000; 2000US-00533559
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expressed sequence tag;
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                                                                                               standard;
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Disclosure; SEQ ID NO 4068; 264pp; English.
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6 Other; Ü, 0 141 G; 150 T; 568 BP; 155 A; 116 C; Sequence

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The invention relates to a method of monitoring (M1) differential expression of multiple genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells, comprises adding fluorescence labeled nucleic acids isolated from the cells to a substrate containing an array of Aspergillus oryzae expressed sequence tag (EST) of AD293898-AD296922, and examining the array under fluorescence excitation conditions. (M1) is useful for monitoring global expression of several genes from a filamentous fungal copen reading frames and monitoring gene copy number variation and stability. In (M1), one spot on an array equals one gene or open reading frame, extensive follow-up characterization is unnecessary since sequence information is available and EST microarrays can be organized based on function of the gene products. This sequence corresponds to an EST sequence of the invention. (Note: this sequence is not given in the printed specification but can be obtained in electronic form from the printed specification but can be obtained in electronic form from the products. This sequence.)
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568;
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ADZ93589 standard; cDNA; 568
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Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger. Aspergillus oryzae; Trichoderma reesei; identification; recommental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering;
                                      ID NO:3839
    CDNA; 1024
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                            entry)
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    standard;
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                                                                                   Aspergillus
                                      Aspergillus
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               AAF11316;
    AAF11316
AAF113
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niger; recombination;

88

Clausen တွ Kauppinen INC Я, , (NOVO) NOVO NORDISK BIOTECH (NOVO) NOVO NORDISK AS. Shuster 2000-594572/56 Rey MW, Berka RM, WPI;

99US-00273623

22-MAR-1999;

Olsen PB;

fungal cells ells and a cel Monitoring differential expression of genes in filamentous uses fluorescence-labeled nucleic acids isolated from the substrate of expressed sequence tags.

English 3161pp; 1718; Page 87; Claim

274pp; English

Example 11; SEQ ID NO 3839;

onitoring the on potential expression culture reading frame represents ESTs from solated from (). The ESTs advantages over genomic or random cDNA clones including elimination, redundancy as one spot on an array equals one gene or open reading frame and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Trichoderma reesei, which are all specifically claimed in the process invention the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from ntified and discovered e q in a first filamentous fungal (FF) cell relative to expression and stress in one or more second filamentous fungal cells. Moglobal expression of genes from FF cells allows the production of the microorganisms to be improved. New genes may be discovered in functions of unknown open reading frames can be idergene copy number variation and stability can be monitored. The of genes can be used to study how FF cells adapt to changes is conditions, environmental stress, spore morphogenesis, recomb

The invention relates to a method for monitoring the differential expression of genes in a first filamentous fungal cell relative to the same genes in one or more second filamentous fungal cells. The method involves differentially labeling nucleic acids from the first and second fungal cells with fluorescent reporter dyes, and adding the mixture of fungal cells with fluorescent reporter dyes, and adding the mixture of funcacently labeled polynucleotides to a substrate containing an array. Of Fusarium venenatum expressed sequence tags (BSTS) selected from ADDISISPADUSSOBS under conditions that permit hybridization. Relative expression of genes in the fungal cells is determined by fluorescence; the fluorescent signal emitted when labeled nucleic acids from the first fungal cell bind to the ESTS in the array differs in color from the first combined fluorescence emission color is produced. The filamentous fungal cell hybridise. When both sets of labeled nucleic acids bind to the array, a distinct combined fluorescence emission color is produced. The filamentous fungal cells, Mucor, Myceliophtora, Neurospora, Penicillium, Thielavia, Tolypocladium, and Trichoderma cells, preferably Fusarium venenatum, Aspergillus niger, or Aspergillus oryzae. The method of the invention is useful for monitoring the expression of a plurality of genes in filamentous fungal cells, in order to improve the cells' procein production capacity when such organisms are used for the industrial production capacity when such organisms are used for the industrial captured from Aspergillus niger strain Bo-95 which were obtained in an example of the invention. Note: The sequence data for this in electronic format directly from the US patent of fice at an electronic format directly from the US patent of sequence data for this electronic format directly from the US patent of the sequence data for this electronic format directly electronic format directly from the US patent directly sequence data for the printed sequence data for the sequence data for

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Sequence 1024 BP;

seqdata.uspto.gov/sequence.html?DocID=US20040222367.

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Monitoring differential expression of genes in a filamentous fungal celrelative to expression of the genes in second filamentous fungal cells, comprises using microarrays containing Fusarium venenatum expressed
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Matches 20; Conservative 0; Mismatches 2;
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Search completed: January 9, 2006, 18:38:56 Job time : 329 secs

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Database

3319 CPEST.449 1899 CPEST.044 1914 CPEST.044 1900 CPEST.045 1911 CPEST.052 1911 CPEST.052 1911 CPG2716B 1385 AJ797385 527 CPG0679B 1207 Cryptospo 630 wlm96.pk0 519 AU066519 104 FP-7 G03. 855 altr212xe 855 altr212xe 855 altr212xe 870 FP-5 C09. 056 PLATE 12 209 AU010089 903 C8h04a1.f Description AA16789 AA16791 AA16791 AA16791 AA16791 AA79738 AQ25452 AJ5632 AJ5632 AJ5632 AJ5632 DR04510 DR04651 DR04487 BM95905 AU01008 AA78390 CO14968 SUMMARIES AA532319 AA167914 AA167914 AA167911 AA167911 AA167911 AA167911 AA167911 AA167911 AA797385 AQ254527 CPA563207 CPA563207 CPA563207 CPA685630 AU066519 BE430105 DR044870 BM959056 AU014209 AA783903 CC149687 254 461 485 520 566 737 737 770 593 907 771 895 1110 518 520 531 Length 1000.0 10 Query Match Score 22444444444 Result No. 0 0 0 0 0 0 0 0 0 0 000000

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(Atlanta, Georgia). Poly A+ RNA was separated from total C. parvum RNA using the Poly(A) Quik mRNA Isolation Kit from Stratagene. Directional CDNA was synthesized by first-strand priming with a Xho I-oligo d(T) linker-primer, second-stranding with RNase H and DNA polymerase I, ligation of EcoR I linkers, and digestion with Xho I, all using the Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned into the EcoR I and Xho I sites of Lambda Uni-ZAP XR vector; the unamplified library was of Lambda Uni-ZAP XR vector; the unamplified library was clones. PCR analysis of 20 random clones indicated that the average insert size was ca. 1.1 kb."
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/db_xref="taxon:5807"
/dev_stage="sporozoite"
/lab_host="E. coli XL1 Blue MRF' Kan"
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/note="Vector: UniZAP XR; Site_1: EcoR I; Site_2: Xho I;
/rotal RNA was isolated from purified Cryptosporidium
parvum sporozoites using TRIZOL reagent (GIBCO-BRL).
Directional cDNA was synthesized by first-strand priming
with a Xho I-oligo d(T) linker-primer, second-stranding
with RNase H and DNA polymerase I, ligation of EcoR I
linkers, and digestion with Xho I, all using the
Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned
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Fax: 415 206 8846
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling
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similar to Cryptosporidium parvum 18S ribosomal RNA gene,
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Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California,
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Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.

1 (bases 1 to 427)
Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum genom expressed sequence tag and genome survey sequence analymol. Biochem. Parasitol. 107 (1), 1-32 (2000)
                                                                                                                                                                                                                                                                                                                                                   core 23; DB 1; Length 254;
red. No. 2.7;
Mismatches n. r-`-
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/mol_type="mRNA"
/strain="IOWA"
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Seq primer: M13 reverse
H1gh quality sequence stop: 461.

Location/Qualifiers

1. .461.

Location/Qualifiers

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Acramism="Cryptosporidium parvum"

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/dav xrefe="taxon:5807"

/dev stage="sporozoite"

/dav stage="sporozoite"

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/note="vector: UnizAP XR; Site_1: EcoR I; Site_2: Xho I;

/clone lib="unizAPCPIOWAsporoLib1"

/note="vector: UnizAP XR; Site_1: EcoR I; Site_2: Xho I;

/rotal RNA was isolated from purifited cryptosporidium

parvum sporozoites using TRIZOL reagent (GIBCO-BRL).

Directional cDNA was synthesized by first-strand priming

with a Xho I-oligo d(T) linker-primer, second-stranding

with RNase H and DNA polymerase I, ligation of EcoR I

linkers, and digestion with Xho I, all using the

Stratagene ZAP-CDNA synthesis kit. The cDNA was cloned

into the EcoR I and Xho I sites of Lambda Uni-ZAP XR

vector; the primary library was >97% recombinant and

contained 1.3 X 10(6) independent clones with an ca.

average insert size of 1.3 kb. Based on open reading frame
into the EcoR I and Xho I sites of Lambda Uni-ZAP XR vector; the primary library was >97% recombinant and contained 1.3 X 10(6) independent clones with an ca. average insert size of 1.3 kb. Based on open reading frame (orf) analysis of the first 64 sequence tags we estimate that up to one-third of the library is composed of genomic DNA clones since approximately 15% of the orfs were incorrectly oriented on the antisense strand."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA167914 LonizaPCpIOWAsporoLib1 Cryptosporidium parvum cDNA 5' similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA
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Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5'
the insert, to correct miscalled bases and assign uncalled (N)
bases throughout the sequence, and to terminate when base-calling
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Preliminary profile of the Cryptosporidium parvum genome: a expressed sequence tag and genome survey sequence analysis Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)

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Contact: Nelson, R. G.

Depts. of Medicine & Pharmaceutical Chemistry

San Francisco General Hospital-University of California, Sa
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Cryptosporidiidae; Cryptosporidium.
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Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' (the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling
                                                                                                                                                                                                                                                     AA167900
CPEST.045 uniZAPCpIOWAsporoLibl Cryptosporidium parvum cDNA 5'
similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA
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Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum genome: expressed sequence tag and genome survey sequence analysi Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
       (orf) analysis of the first 64 sequence tags we that up to one-third of the library is composed DNA clones since approximately 15% of the orfs wincorrectly oriented on the antisense strand."
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Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida
Cryptosporidiidae, Cryptosporidium.
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                                                                                            DB 1; Length 461; 2.9;
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Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Cryptosporidium parvum"
/mol_type="mRNA"
/strain="IOWA"
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                                                                                            100.0%; Score 23; DE 100.0%; Pred. No. 2.5; ive 0; Mismatches
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Seq primer: M13 reverse
High quality sequence stop: '
Location/Qualifiers
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COMMENT

SOURCE

RESULT

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/db_xref="LOWA"
/db_xref="Lowa"
/dcv_stage="sporozoite"
/dev_stage="sporozoite"
/lab_host=="Coli XL1 Blue MRF' Kan"
/clone lib="unizAPCpIOWAsporoLib1"
/note="Vector: UnizAP XR; Site_1: EcoR I; Site_2: Xho I;
/rotal RNA was isolated from purified Cryptosporidium
parvum sporozoites using TRIZOL reagent (GIBCO-BRL).
Directional cDNA was synthesized by first-strand priming
with a Xho I-oligo d(T) linker-primer, second-stranding
with RNase H and DNA polymerase I, ligation of EcoR I
linkers, and digestion with Xho I, all using the
Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned
into the EcoR I and Xho I sites of Lambda Uni-ZAP XR
vector; the primary library was >97% recombinant and
contained 1.3 x 10(6) independent clones with an ca.
average insert size of 1.3 kb. Based on open reading frame
(orf) analysis of the first 64 sequence tags we estimate
that up to one-third of the library is composed of genomic
DNA clones since approximately 15% of the orfs were
incorrectly oriented on the antisense strand."
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Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalled bases and assign uncalled (N)
bases throughout the sequence, and to terminate when base-calling became ambiguous.
Seq primer: M13 reverse
High quality sequence stop: 520.
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CpEST.003 uniZAPCpIOWAsporoLibl Cryptosporidium parvum cDNA 5'
similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA
sequence.
AA167911
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Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriii
Cryptosporidiidae; Cryptosporidium.

1 (bases 1 to 520)
Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum gesexpressed sequence tag and genome survey sequence and Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Cryptosporidium parvum"
/mol_type="mRNA"
/strain="IOWA"
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    100.0%;
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RESULT 6 AA167858/c

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Matches

DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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/organism="Cryptosporidium parvum"
//organism="Cryptosporidium parvum"
//mol_type="genomic DNA"
//ab_rost="10WA"
//ab_host="E. coli XL2 Blue MRF'"
//lab_host="E. coli XL2 Blue MRF'"
//lab_host="E. coli XL2 Blue MRF'"
//clone_lib="CpIOWAgDNA1"
//note="Vector: pBlueScript II (SK-); Site_l: EcoRV; C.
parvum (IOWA isolate) genomic DNA was hydrodynamically
sheared to produce fragments having a tight size
distribution between 2-4 kb by Dr. Yvonne Thorstenson of
the Stanford DNA Sequencing and Technology Center
(http://sequence-www.stanford.edu/group/techdev/shear.htm)
. The randomly sheared gDNA was chromatographed on
Sephacryl S-400 to remove any small fragments and DNA
eluting in the void volume was subcloned into an EcoR
V-digested, alkaline phosphatase-treated pBlueScript II
(SK-) vector and transformed into E. coli strain XL2 Blue
MRF'. Recombinant clones from the first plating of the
library were selected for sequence analysis using T3 and
T7 primers."
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similar to C.
sequence.
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AJ797385 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018 4 01 108, mRNA sequence.
AJ797385
AJ797385.1 GI:51112713
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Seg primer: T3
                                                                                                                                                                                                                                                                     Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.

Cryptosporidiidae; Cryptosporidium.

Cryptosporidiidae; Cryptosporidium.

Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum genome: ar expressed sequence tag and genome survey sequence analysis

Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)

10717299

Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, Sar
                                                                                                                                                                                                                                                                                                                                                                                                                                 genome:
analysis
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red. No. 3.1;
Mismatches 0; Indela
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AQ935911.1 GI:6638124
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                                                                                                                       737 bp
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Class: shotgun
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AJ797385/c
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// barate="lowA"
// dev_stage="sporozoite"
// dev_stage="sporozoite"
// lab_host="B. coli XL1 Blue MRF' Kan"
// clone_lib="uniZAPCDIOWAsporoLib1"
// note="Vector: UniZAP XR; Site_1: EcoR I; Site_2: Xho I;
// note="Vector: UniZAP XR; Site_1: EcoR I; Site_2: Xho I;
// note="Vector: UniZAP XR; Site_1: EcoR I; Site_2: Xho I;
// Total RNA was isolated from purified Cryptosporidium
parvum sporozoites using TRIZOL reagent (GIBCO-BRL).
Directional CDNA was synthesized by first-strand priming
with a Xho I-oligo d(T) linker-primer, second-stranding
with RNase H and DNA polymerase I, ligation of EcoR I
linkers, and digestion with Xho I, all using the
Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned
into the EcoR I and Xho I sites of Lambda Uni-ZAP XR
vector; the primary library was >97% recombinant and
contained 1.3 X 10(6) independent clones with an ca.
average insert size of 1.3 kb. Based on open reading frame
(orf) analysis of the first 64 sequence tags we estimate
that up to one-third of the library is composed of genomic
DNA clones since approximately 15% of the orfs were
incorrectly oriented on the antisense strand."
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Tel: 415 206 8846

Fax: 415 206 3353

Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5'
the insert, to correct miscalled bases and assign uncalled (N)
bases throughout the sequence, and to terminate when base-calling
became ambiguous.
Seq primer: M13 reverse
High quality sequence stop: 566.
                                                                                                                                                                                           CpEST.052 uniZAPCpIOWAsporoLib1 Cryptosporidium parvum cDNA 5' similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA 8A167858
AA167858
AA167858.1 GI:1746091
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimer Cryptosporidiidae; Cryptosporidium.

Cryptosporidiidae; Cryptosporidium.

(bases 1 to 566)
Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum expressed sequence tag and genome survey sequence Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
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    Indels
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Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of
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/mol_type="mRNA"
/strain="IOWA"
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                                                    1 CCGTAAAGTTATTATGAGTCACC 23
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FEATURES

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Query Match Best Local S Matches 23

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nes 23; Conser
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Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Seq primer: T3
Class: shotgun.
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       Antirrhinum majus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae,
Antirrhinum.
                                                                                                                  Sommer, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Californi
                                                                                                                                                 and
                                                                                                           Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Saedler, H. and Zachgo, S.
Characterization of Antirrhinum Petal Development and Identification of Target Genes of the Class B MADS By DEFICIENS
Plant Cell 16 (12), 3197-3215 (2004)
15539471
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           759;
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CpG0679B CpIOWAgDNA1 Cryptosporidium parvum genomic
parvum ribosomal RNA gene, genomic survey sequence.
AQ254527
                                                                                                                  Fellenberg, K., Schwarz-Sommer, Z
                                                                                                                                                                                                                                                                                                                                     /organism="Antirrhinum majus"
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_4_01_108"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimer Cryptosporidium.

Cryptosporidiidae; Cryptosporidium.

(bases 1 to 770)
Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum expressed sequence tag and genome survey sequence Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
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Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Cryptosporidium parvum"
/mol_type="genomic DNA"
/strain="IOWA"
/db_xref="taxon:5807"
/lab_host="E. coli XL2 Blue MRF'"
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red. No. 3.1;
Mismatches
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Antirrhinum majus (snapdragon)
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AQ254527/c
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/clone_lib="CplOWAgDNA1"
/note="Vector: pBlueScript II (SK-); Site_l: EcoRV; C.
parvum (10WA isolate) genomic DNA was hydrodynamically
sheared to produce fragments having a tight size
distribution between 2-4 kb by Dr. Yvonne Thorstenson of
the Stanford DNA Sequencing and Technology Center
(http://sequence-www.stanford.edu/group/techdev/shear.htm)
. The randomly sheared gDNA was chromatographed on
Sephacryl S-400 to remove any small fragments and DNA
eluting in the void volume was subcloned into an EcoR
v-digested, alkaline phosphatase-treated pBlueScript II
(SK-) vector and transformed into E. coli strain XL2 Blue
MRF'. Recombinant clones from the first plating of the
library were selected for sequence analysis using T3 and
T7 primers."
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Integrated mapping, chromosomal sequencing and sequence analysis of Cryptosporidium parvum
Genome Res. 13 (8), 1787-1799 (2003)
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T7 end
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2 (bases 1 to 593)
Dear, P.H.
Direct Submission
Submitted (09-MAY-2003) Dear P.H., PNAC Biotech Division, MRC
Submitted (09-MAY-2003) Dear P.H., PNAC Biotech Division, MRC
Laboratory of Molecular Biology, Hills Road, Cambridge, Cambs CB2
2QH, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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Cryptosporidium parvum
Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
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1. .593
/organism="Cryptosporidium parvum"
/mol_type="genomic DNA"
/serotype="Type 2"
/isolate="Iowa"
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28;
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Pred. No. 28;
0; Mismatches
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Cryptosporidium parvum GSS, PAC clesequence, genomic survey sequence.
AJ563207
AJ563207.1 GI:31338027
GSS; genome survey sequence.
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/clone="pica_0014_e03"
/clone_lib="pica"
/dev_stage="oocyst"
/note="T7_end_sequence"
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Triticum aestivum (bread wheat)

Triticum aestivum

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Booideae; Triticeae; Triticum.

I (bases 1 to 558)

Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T.,

Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A.,

Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J.,

Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P.,

Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G.,

Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.

International Triticeae EST Cooperative (ITEC): Production of

Expressed Sequence Tags for Species of the Triticeae

L Unpublished (2000)
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HS-5 by a
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                                                                                                                                                                          /db_xref="taxon:108458"
/clone="NaEX96-67"
/clone_lib="Chlamydomonas sp. HS-5 lambda ZAP II"
/note="Vector: lambda ZAP II; The cDNA clone was is from the halotolerant green alga Chlamydomonas HS-5 functional expression screening in E.coli cells. The principle of the screening method was based on the acquisition of stress tolerance of the bacterial cearrying the cDNA."
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           Amagasaki,
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Fax: 306 975 4839
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International Triticeae EST Cooperative
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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Pred. No. 57;
0; Mismatches
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db_xref="taxon:4565"
clone="TAS007.B02"
clone_lib="ITEC_TAS_Wheat
                                                                                                      'organism="Chlamydomonas
'mol_type="mRNA"
'strain="HS-5"
           Bio-Laboratory; Nakoji
Center, Blocation/Qualifiers
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CDNA clone TAS007.B02,
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ilarity 91.3%;
Conservative (
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[larity 95.5%;
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 907)
Miyasaka, H., Kanaboshi, H. and Ikeda, K.
Isolation of several anti-stress genes from halotolerant gre Chlamydomonas by a simple functional expression screening in Unpublished (1999)
Contact: Kazunori Ikeda
Environmental Symbiosis section
Kansai Environmental Engineering Center Co.Ltd
3-5 Adzuchimachi 1-Chome Chuo-ku, Osaka, Osaka 541-0052, Jap Email: daike@mb.infoweb.ne.jp
NaCl inducible;
Present address: The Kansai Electric Power Co., Technical Ref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                   eae;
                                                                                                                                                                                             Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

I (bases 1 to 539)

Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Y
Miao, G., Caraher, N. and Hanafey, M.K.

DuPont Wheat cDNA Sequence
Unpublished (2002)

Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company
I Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, US

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n.
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KhoI; Wheat (Triticum aestivum L.) seedlings Sinoculation w/ E. graminis"
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AU066519 Chlamydomonas sp. HS-5 lambda Zł
HS-5 cDNA clone NaEX96-67, mRNA sequence.
AU066519
AU066519.1 GI:6448304
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/mol_type="mRNA"
/cultivar="Stephens"
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Pred. No. 54;
0; Mismatches
                                                wlm96.pk030.j22 wlm96 Triticum ae 5.39 bp 5. end, mRNA sequence. CA685630 CA685630.1 GI:25274269 EST. Triticum aestivum (hread triticum aestivum aestivum aestivum (hread triticum aestivum 
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Chlamydomonas sp. HS-5
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Location/Qualifiers
1. .769
/organism="Triticum aestivum/Phaeosphaeria nodorum mixed
EST library"
/mol_type="mRNA"
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/dev_stage="Sporulation"
/clone_lib="cDNA library of sporulating Phaeosphaeria
nodorum SN15 on Wheat cv. Amery"
/note="Vector: pTriplex2; Total RNA was extracted from P.
nodorum strain SN15 infected wheat cv. Amery at 14 dpi.
Library contains both fungal and plant sequences."
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ler conditions
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FP-7 G03.SEQ cDNA library of sporulating Phaeosphaeria nodorum SN15 on Wheat cv. Amery Triticum aestivum/Phaeosphaeria nodorum mixed EST library cDNA, mRNA sequence.
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Alternaria brassicicola
Alternaria brassicicola
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.

(bases 1 to 771)
Crawer, R.A., Craven, K.D., Thon, M.R., Cho, Y., Knudson, D.L.,
Mitchell, T.K. and Lawrence, C.B.
Expressed Sequence Tag (EST) Analysis of a Compatible Alternaria brassicicola-Brassica oleracea Interaction
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Triticum aestivum/Phaeosphaeria nodorum mixed EST library
Eukaryota; mixed EST libraries.

1 (bases 1 to 769)
5 Lowe, R.G.T. and Oliver, R.P.
Sporulation of Phaeosphaeria nodorum SN15
Contact: Richard Oliver
Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
Murdoch University
South Street, Murdoch, W.A 6150, Australia
Tel: +0893607404
Email: roliver@murdoch.edu.au.
                                                                                                                                                                                                                                                                                                                                                                                                                      (ACNFP)
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altr212xe11 A. brassicicola mycelial culture grown undof Nitrogen Starvation Alternaria brassicicola cDNA claltr212xe11, mRNA sequence.
DN476855
DN476855.1 GI:60674166
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Center for Integrated Fungal Research, NC State Univer
851 Main Campus Dr. Suite 233, Raleigh, NC 27606, USA
Tel: (919) 513-3926
Fax: (919) 513-0024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 769;
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CCGTAAAGTTATCATGAATCACC 368
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grown under
                                                           /organism="Alternaria brassicicola"
/wol_type="mRNA"
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/note="Vector: pGEMt; Mycelial culture grown unconditions of Nitrogen Starvation."
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Seq primer: T7 SP6 primer.
Location/Qualifiers
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/cgn2_6/ptodata/1/ina/RE_COMB.seq:* Patents ssued Database

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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DB DB

Minimum Maximum

printed Ø Pred. No, is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.

SUMMARIES

					SOMMAKIES	
		æ				
Result No.	Score	Query Match	Length	DB	ID	escriptio
1		1	1750	. 6	US-08-949-770-1	Sequence 1, Appli
	18.	Ø	439	~	US-08-093-144-3	, Appl
	18.	81.7	444	N	US-08-093-144-6	6, Appl
Ω 4	18.8	81.7	446	~	US-08-093-144-4	4, App
	18.	81.7	568	ო	-40	4068,
	18.	81.7	02	ო	-533-559-383	383
	18.	81.7	2055	ო	US-10-121-740-3	3, App
	18.	, ,	08	ന	US-10-121-740-1	1, App
	18.	6	709	ო		281, Ap
7	17.	~	1102	ጥ	US-10-037-417-43	Sequence 43, Appl
-	17.		10	ო	US-10-037-417-45	45, App
7	17.	5	601	ო	-949-016-1216	1216
c 13	17.	2	601	ო	-016-1216	1216
	17.	رى	601	ო	-949-016-16526	16526
Н	17.	S.	601	ო	-016-1652	165
٦	17.	ъ.	526	ო	-09-949-01	12797,
7.7	17.	ū.	35263	ო	-09-949-016-1639	equence 16399,
-	17.	5.	973	m	덖	_
c 19	17.	4	4	~	-09	equence 5, Ap
~	17.	4.	0	ო	-17	
21	-	74.8	723	٣	-08-998-41	equence 952,
c 22	17.	4.		ო	US-09-805-127-7	7, Appl
N	17.	4.	~	m	-710	equence 1, Appl
C 24	17.	4.	1788	~	US-08-867-820A-1	Sequence 1, Appli

equence 14	e 14205,	9, App	e 45, App	equence 45, App	equence 45, App	equence 45, App	equence 13451	157835,	equence 16144	equence 14145	equence 14145	1453	equence 119, Ap	, App	equence 3, Appl	equence 3, Appl	312,	equence 11820,	equence 1	e 15753,
US-09-949-016-14018	-016-1420	-09-265-58	US-09-186-276B-45	-08-842-445-4	-09-186-188B-4		-09-949-016-1345	9-016-1578	-09-949-01	-09-949-016-14145	-09-949-016-14	-09-949-016-14145	7-11	-09-489-847-5	-08-469-4	-07-890-609-3	-949-016-1631	-949-016-1182	-949-016-171	9-016-1575
73.0 92505	73.0 130971	72.2 409	72.2 1279	72.2 1279	72.2 1279	72.2 1279	72.2 139562	71.3	71.3 191433	70.4 601	70.4 601	70.4 601	70.4 2059	70.4 2076	70.4 22846	70.4 22846	70.4 25122	70.4 192700	70.4 192704	.4 236964
5 1	26 1	7	28 1	29	30	31 1	32	3	34 1	35 1	36 1	37 1	38 1	39 1	40 1	41 1	42 1	43 1	44	45 16.

ALIGNMENTS

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Nucleic Acid Sequence Amplification
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RESULT 1
US-08-949-770-1/C

i Sequence 1, Application US/08949770

j Patent No. 6063604

i GENERAL INFORMATION:
APPLICANT: Wick, James F.
APPLICANT: Blassak, Michele
APPLICANTE Target Nucleic Acid Sequence Amp
CORRESPONDENCES:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & E
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
CITY: Chicago
STARTE: Illinois
COUNTRY: United States of America
ACONTRY: United States of America
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,770
FILING DATE:
CLASSIFICATION NUMBER: 08/617,045
FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ANAW: POCCHANIAN DATA:
ATTORNEY/AGENT INFORMATION:
ANAM: POCCHANIAN DATA:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ANAM: POCCHANIAN DATA:
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ANAM: POCCHANIAN DATA:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AG
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South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 28003/33045
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-648
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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SIMON, LUC
LALONDE, MAURICE
VENTION: DNA PROBES FOR THE DETECTION
VENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR THE DETECTION OF ENDOMYCORRHIZAL FUNGI
                                                                                                                                                                                                                                                       Version #1.25
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R: LAH/3122/92223/MJW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.8; D
Pred. No. 17;
0; Mismatches
                                                                                                                L. Street,
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                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/093,144
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-093-144-4/c
; Sequence 4, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOI
; TITLE OF INVENTION: ARBUSCULAR ENI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hymo, Lawrence A.
REGISTRATION NUMBER: 19,057
REFERENCE/DOCKET NUMBER: LAH/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                SEE: CUSHMAN, DARBY & C
Eleventh Floor, 1615
Washington
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90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 444 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: CUSHMAN, DARE
: Eleventh Floor,
Washington
                                                                                                                                         STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
      APPLICANT: SIMON, LUC
APPLICANT: LALONDE, MAUR
TITLE OF INVENTION: DNA
TITLE OF INVENTION: ARBU
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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20; Conser
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CITY: WASTATE: 1
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STATE:
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Best Local
Matches 2
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                         Cryptosporidium
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                                                                                                                  Indels
                                                                                   Length
                                                                                                                                                                                                                                                                   Patent No. 5434048
GENERAL INFORMATION:
APPLICANT: SIMON, LUC
APPLICANT: LALONDE, MAURICE
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                    DB 3
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Pred. No. 17;
0; Mismatches
                        of
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: Eleventh Floor, 1615 L. Street, CITY: Washington STATE: D.C.
                                                                                                                 Mismatches
                                                                                    23;
No.
                          gene
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15-AUG-1991
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Pred.
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US/08/093,14
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                                                                                                                                                              Sequence 6, Application US/08093144
Patent No. 5434048
GENERAL INFORMATION:
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US-08-093-144-3/c
; Sequence 3, Application US/08093144
· Datent No. 5434048
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NAME: Hymo, Lawrence A.
REGISTRATION NUMBER: 19,057
                      /= "18s
parvum"
                                                                                    100.0%;
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ilarity 90.9%;
Conservative
      ; NAME/KEY: misc feature
; OTHER INFORMATION: /= '
; OTHER INFORMATION: part
US-08-949-770-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 base pairs nucleic acid
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA APPLICATION NUMBER: U
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                                                       Query Match
Best Local Similarity
...t.hes 23; Conserva
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Matches 20; Conser
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US-08-093-144-6/c
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Gaps

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APPLICANT: Randy M. Berka
APPLICANT: Randy M. Berka
APPLICANT: Jeffrey R.Shuster
APPLICANT: Jeffrey R.Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 18;
0; Mismatches
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Pred. No. 17;
0; Mismatches
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US-10-121-740-1/c
; Sequence 1, Application US/10121740
; Patent No. 6911338
; GENERAL INFORMATION:
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illarity 90.9%;
Conservative
                                                                                                                                                                                                                                                                                                                FEATURE:

NAME/KEY: misc_feature

LOCATION: (1) ... (1024)

OTHER INFORMATION: n = A,T,C
US-09-533-559-3839
                                                                                                                                                                                                                                                                                                                                                                                                                th 81.7%;
Similarity 90.9%;
20; Conservative
                                                                                                                                                                                                                                                                                                   ORGANISM: Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Muscodor roseus
US-10-121-740-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-121-740-3/c
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2055
                                                                                                                                                                                                                                                    SEQ ID NO 3839
LENGTH: 1024
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Best Local S
Matches 20
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Matches 2
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                                                                                                                                                                                                                                                                                                                                       Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4068, Application US/09533559
Sequence 4068, Application US/09533559
Patent No. 6902887
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Joffrey R.Shuster
APPLICANT: Barke Olsen
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT FILING DATE: 2000-03-22
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4068
LENGTH: 568
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Mismatches
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Pred. No. 1
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US-09-533-559-3839/c
; Sequence 3839, Application US/09533559
; Patent No. 6902887
                                                    07/745,192
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                                                 APPLICATION NUMBER: US 07/745
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hymo, Lawrence A.
REGISTRATION NUMBER: 19,057
REFERENCE/DOCKET NUMBER: LAH/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                CGAAAGTTATTATGAATCACC
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TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                      sh 81.7%;
l Similarity 90.9%;
20; Conservative
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                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(568)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                          linear
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les 20; Conser
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Length 1024;
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; Sequence 3, Application US/10121740
; Patent No. 6911338
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT PILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
                                                                                                                             Length 709
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Pred. No. 33;
0; Mismatches
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CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 43
                                                                                                                                                                                                                                        440
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APPLICATION NUMBER: 60/303,231
FILING DATE: 2001-07-05
                                                                                                                                                                                                                                                                                                                           43, Application US/10037417
0. 6903201
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Spytek, Kimberly A
Patturajan, Meera
Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                               Kekuda, Ramesh
Alsobrook II, John F
Tchernev, Velizar T
Liu, Xiaohong
    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1237UP
                                                                                                                             th 79.1%;
Similarity 87.0%;
20; Conservative
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Ellerman, Karen
Malyankar, Uriel I
Rothenberg, Mark
Stone, David J
Boldog, Ferenc L
Guo, Xiaojia
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, Shlomit
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GENERAL INFORMATION:
APPLICANT: Kekuda, Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gorman,
                                                                                                                                                                                                                                                                                                             10-037-417-43/c
                                                                             ; ORGANISM:
US-08-998-416-281
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Matches 20
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SEQ ID NO 4
LENGTH: 1
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APPLICANT:
APPLICANT:
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APPLICANT:
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US-08-998-416-281
i Sequence 281, Application US/08998416
j Patent No. 6239264
j GENERAL INFORMATION:
j APPLICANT: Philippsen, Peter
APPLICANT: Steiner, Sabine
j APPLICANT: Steiner, Sabine
APPLICANT: Wendland, Jurgen
j APPLICANT: Wendland, Jurgen
j APPLICANT: Rebischung, Corinne
j APPLICANT: Rebischung, Corinne
j TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII

TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                              Length 2089;
APPLICANT: Strobel, Gary
APPLICANT: Manker, Denise
TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
TITLE OF INVENTION: USE
FILE REFERENCE: AQ 2019.40
CURRENT APPLICATION NUMBER: US/10/121,740
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/283,902
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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R: PF/5-30306/A/CGC1976
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Pred. No. 18;
0; Mismatches
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
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FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-
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TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
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90.9%;
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LENGTH: 709 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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LENGTH: 2089
TYPE: DNA
ORGANISM: Muscodor albus
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PRIOR APPLICATION DATA:
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nes 20; Conser
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TELEFAX: 915
INFORMATION FOR 5
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TYPE: DNA ORGANISM:
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Matches 18
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FILE REFERENCE: 21402-235

CURRENT APPLICATION NUMBER: US/10/037,417

CURRENT FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: 60/260,360

PRIOR FILING DATE: 2001-01-08

PRIOR FILING DATE: 2001-01-08

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28
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                                                 Score 17.8; D. Pred. No. 51; 0; Mismatches
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)R APPLICATION NUMBER: 60/291,186
)R FILING DATE: 2001-05-15
)R APPLICATION NUMBER: 60/303,231
)R FILING DATE: 2001-07-05
)R APPLICATION NUMBER: 60/305,060
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US-10-037-417-45/c
; Sequence 45, Application US/10037417
; Sequence 45, Application US/10037417
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Shenoy, Suresh G
Anderson, David W
Padigaru, Muralidhara
Taupier Jr, Raymond J
Miller, Charles E
Eisen, Andrew J
                                                                                                                            92 CCGTAAAGTGAGTATGAGTCA
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                                                                                                            CCGTAAAGTTATTATGAGTCA
                                                                                                                                                                                                                Sequence 6903201;
Patent No. 6903201;
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Σ
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Vernet, Corine A.M
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NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 1102
                                                                                                                                                                                                                                                                                                             Spytek, Kimberly P
Patturajan, Meera
Grosse, William M
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                                                  th 77.4%;
Similarity 90.5%;
19; Conservative
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Malyankar, Uriel
Rothenberg, Mark
Stone, David J
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Edinger, Shlomit
Sciore, Paul
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Guo, Xiaojia
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FILING DATE: 2001-09
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                           Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
  ; Trrs: Lanc sapiens; ORGANISM: Homo sapiens
US-10-037-417-43
                                                                                                                                                                                                                                                                                                                                            Grosse,
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                                                     Query Match
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Matches 19
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APPLICANT:
APPLICANT:
APPLICANT:
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TYPE: DNA
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: VENTER: J. Craig et al.
APPLICANT: VENTER: J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 121654
LENGTH: 601
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US-09-949-016-121653/C
US-09-949-016-121653/C

Sequence 121653, Application US/09949016

Fatent No. 6812339
GENERAL INFORMATION:
FATELE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF ESQ ID NOS: 207012

SOFTHERE FASESEQ for Windows Version 4.0

LENGTH: 601
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Pred. No. 76;
0; Mismatches
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Pred. No. 76;
0; Mismatches
Score 17.8; D
Pred. No. 51;
0; Mismatches
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US-09-949-016-121654/c
; Sequence 121654, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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Best Local Similarity 94.7%;
Matches 18; Conservative
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   Query Match
Best Local Similarity
Matches 19; Conser
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; ORGANISM: Human
US-09-949-016-121653
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RESULT 14
US-09-949-016-165267/C
Sequence 165267, Application US/09949016
Sequence 165267, Application US/09949016
Sequence 165267, Application US/09949016
Sequence 165267, Application US/09949016
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207002
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 165267
LENGTH: 601
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US-09-949-016-165268/C

; Sequence 165268, Application US/09949016
; Sequence 165268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; PAPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 165268
; LENGTH: 601
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Matches 18; Conservative
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CRGANISM: Human
US-09-949-016-165268
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Published Applications NA Main: *

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq: *

2: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq: *

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq: *

4: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq: *

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq: *

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10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq: *

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Minimum Maximum Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
	9-954-695-47	9-954-695-53	9-954-695-59	9-954-69	9-954-58	9-954-586-53	9-954-586-59	9-954-586-65	0-653-047-4068	.0-094-097B-112	0-653-047-3839	0-483-439-1	0-121-740-3	.0-623-432-3	.11-131-659-3	.0-121-740-1	.0-623-432-1	.11-131-659-1	.0-062-674-1363	.0-425-115-31251	.0-037-417-43	.0-037-417-45	9-925-065A-384347
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ALIGNMENTS

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Sequence 47, Application US/09954695

Sequence 47, Application US/09954695

Patent No. US20020055116A1

GENERAL INFORMATION:

APPLICANT: CUNNINGHAM, Melissa M.

APPLICANT: STULL, Paul D.

APPLICANT: STULL, Paul D.

APPLICANT: WEISBURG, William G.

TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF

TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE

FILE REFERENCE: GP116-02.UT

CURRENT APPLICATION NUMBER: US/09/954,695

CURRENT FILING DATE: 2001-09-12

PRIOR FILING DATE: 2000-09-12

NUMBER OF SEQ ID NOS: 69

SOFTWARE: Patentin version 3.1

SEQ ID NO 47

LENGTH: 23
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US-09-954-695-53/c
US-09-954-695-53/c
; Sequence 53, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
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ORGANISM: Artificial
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Sequence 53, Application US/09954586

Batent No. US20020146717A1

GENERAL INFORMATION:

APPLICANT: CUNNINGHAM, Melissa M.

APPLICANT: STULL, Paul D.

APPLICANT: WEISBURG, William G.

TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRES;

TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE

FILE REFERENCE: GP116-03.UT

CURRENT APPLICATION NUMBER: US/09/954,586

CURRENT FILING DATE: 2001-09-11

PRIOR FILING DATE: 2000-09-12

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PatentIn version 3.1
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APPLICANT: CUNNINGHAM, Melissa M.
APPLICANT: WEISBURG, William G.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRES;
TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE;
FILE REFERENCE: GP116-03.UT
CURRENT APPLICATION NUMBER: US/09/954,586
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/232,028
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.1
SEQ ID NO 47
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Patent No. US20020146717A1
GENERAL INFORMATION:
APPLICANT: CUNNINGHAM, Melissa M.
APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
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llarity 69.6%;
Conservative 7
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                                                 Sequence
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                                                                               Synthetic
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ORGANISM: Artificial
FEATURE:
             LENGTH: 23
TYPE: RNA
ORGANISM: Artificial
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16; Conser
                                                                                OTHER INFORMATION:
-09-954-695-65
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-09-954-586-47/c
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US-09-954-586-53/c
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ENGTH: 23
SEQ ID NO 65
LENGTH: 23
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Matches 16
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APPLICANT: CUNNINGHAM, Melissa M.
APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
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APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
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Pred. No. 1.
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CURRENT APPLICATION NUMBER: US/09/954,695
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/232,028
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.1
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CURRENT APPLICATION NUMBER: US/09/954,69
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/232,028
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.1
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                 60/232,028
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US-09-954-695-59
; Sequence 59, Application US/09954695
; Patent No. US20020055116A1
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Patent No. US20020055116A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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              PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-09-12 NUMBER OF SEQ ID NOS: 69 SOFTWARE: Patentin version 3.1
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Best Local Similarity
Matches 23; Conser
 FILING DATE:
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                                                                SOFTWARE: Pa
SEQ ID NO 53
LENGTH: 23
                                                                                                                    TYPE: RNA
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Best Local
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RESULT 10
US-10-094-097B-112/c
is Sequence 112, Application US/10094097B
is Publication No. US20030185840A1
is Fublication No. US20030185840A1
is APPLICANT: IOANNIDES, CONSTANTIN G.
is APPLICANT: PEOPLES, JR., GEORGE E.
it TITLE OF INVENTION: BINDING PROTEIN
if TILE OF INVENTION: BINDING PROTEIN
if FILE REFERENCE: AM-PO2120USI / UTSC:686US
is CURRENT APPLICATION NUMBER: US/094,097B
is CURRENT PILING DATE: 2002-03-08
is PRIOR FILING DATE: 2001-03-08
is PRIOR APPLICATION NUMBER: 60/274,676
is PRIOR APPLICATION NUMBER: 60/274,676
is PRIOR APPLICATION NUMBER: 2001-03-09
is NUMBER OF SEQ ID NOS: 269
is SOFTWARE: Patentin Ver. 2.1
is SEQ ID NO 112
is LENGTH: 685
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APPLICANT: Randy M. Rey
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Jeffrey R.Shuster
APPLICANT: Jeffrey R.Shuster
APPLICANT: Barai Kauppinen
APPLICANT: Beter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4068
LENGTH: 568
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Pred. No. 1.6e+02;
0; Mismatches 2;
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 Mismatches
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US-10-653-047-4068/c
; Sequence 4068, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
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; LOCATION: (1)...(568)
; OTHER INFORMATION: n = A,T,C
US-10-653-047-4068
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Best Local Similarity 90.9%;
Matches 20; Conservative
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ORGANISM: Aspergillus niger
  Conservative
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APPLICANT: STULL, Paul D.
APPLICANT: STULL, Paul D.
APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE FILE REFERENCE: GP116-03.UT CURRENT APPLICATION NUMBER: US/09/954,586
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/232,028
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2001-09-11
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        Synthetic Construct
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APPLICANT: WEISBURG, William G.
TITLE OF INVENTION: COMPOSITIONS,
TITLE OF INVENTION: CRYPTOSPORIE
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                                                         th 100.0%;
Similarity 100.0%;
23; Conservative (
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SOFTWARE: PatentIn version
SEQ ID NO 65
LENGTH: 23
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PRIOR FILING DATE: 2000-0

    Application U
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Best Local Similarity
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US-09-954-586-59
        ; OTHER INFORMATION:
US-09-954-586-53
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LENGTH: 23
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Patent No. U
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APPLICANT: Strobel, Gary
APPLICANT: Manker, Denise
TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
TITLE OF INVENTION: USE
FILE REFERENCE: AQ 2019.40
CURRENT APPLICATION NUMBER: US/10/623,432
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 60/283,902
PRIOR FILING DATE: 2002-04-11
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS
TITLE OF INVENTION: USE
FILE REFERENCE: AQ 2019.40
CURRENT APPLICATION NUMBER: US/10/121,740
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/283,902
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2001-04-16
                                                                                                           Score 18.8; DB 9;
Pred. No. 1.8e+02;
); Mismatches 2
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Pred. No. 1.9e+02
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version
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Publication No. US20030186425A1
GENERAL INFORMATION:
APPLICANT: Strobel, Gary
APPLICANT: Manker, Denise
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; ORGANISM: Muscodor roseus
US-10-623-432-3
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                                      TYPE: DNA
ORGANISM: MPC1005
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ENGTH: 2055
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Sequence 3839, Application US/10653047

Publication No. US20040229367A1

GENERAL INFORMATION:

APPLICANT: Randy M. Berka

APPLICANT: Michael W. Rey

APPLICANT: Jeffrey R.Shuster

APPLICANT: Jeffrey R.Shuster

APPLICANT: Jeffrey R.Shuster

APPLICANT: Deter Bjarke Olsen

ITILE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

FILE REFERENCE: 5849.200-US

CURRENT APPLICATION NUMBER: US/10/653,047

CURRENT APPLICATION NUMBER: US/09/533,559

PRIOR FILING DATE: 2000-03-22

PRIOR FILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 7860

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3839

LENGTH: 1024
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                                                        Score 18.8; DB 6;
Pred. No. 1.6e+02;
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Pred. No. 1.7e+02;
0; Mismatches 2;
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TITLE OF INVENTION: SH3 DOMAIN BINDING INHIBITORS
FILE REFERENCE: 09859/0200055-USO
CURRENT APPLICATION NUMBER: US/10/483,439
CURRENT FILING DATE: 2004-01-09
PRIOR APPLICATION NUMBER: PCT/JP02/03932
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
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US-10-483-439-1/c;
Sequence 1, Application US/10483439;
Publication No. US20050069999A1;
GENERAL INFORMATION:
APPLICANT: Sharma, Sreenath V.
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Matsushita, Noriko
Ando, Katsuhiko
Yoshida, Chitose
Nakano, Hirofumi
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    ; OTHER INFORMATION: N
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US-10-653-047-3839/c
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US-11-131-659-3/C
; Sequence 3, Application US/11131659
; Publication No. US20050220769A1
; GENERAL INFORMATION:
    APPLICANT: Strobel, Gary
    APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
    TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019-40
; CURRENT FILING DATE: 2002-03-11
; PRIOR FILING DATE: 2002-03-11
; PRIOR FILING DATE: 2002-03-11
; PRIOR FILING DATE: 2001-04-16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Muscodor roseus
US-11-131-659-3
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Pred. No. 1.9e+02;
); Mismatches 2;
 Score 18.8; DB 7;
Pred. No. 1.9e+02;
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SUMMARIES		ID		-10-519-	US-11-112-908-44	-11-112-	-10-750-	-10-750-6	-10-750-	-10-750-	-10-750-	-10-750-6	-10-750-	-10-750-62	-10-750-	-10-750-	-10-750-1	-10-750-	-10-750-	-10-750-	-11-102-9	•	-10-750-6	1-121-	0-995-	-750-	
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                                                              Sequence 1, Application US/10519379
Sequence 1, Application US/10519379
Publication No. US20050255126A1
GENERAL INFORMATION:
APPLICANT: ASAHI DENKA Co., Ltd.
TITLE OF INVENTION: microorganism and method for producing:
TITLE OF INVENTION: microorganism
FILE REFERENCE: A0301
CURRENT APPLICATION NUMBER: US/10/519,379
CURRENT FILING DATE: 2004-12-27
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 1
LENGTH: 1732
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; ORGANISM: Aureobasidium pullulans ADK-34
US-10-519-379-1
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APPLICANT: KERR, KILLING APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN Version 3.1
SEQ ID NO 35778
LENGTH: 848
LENGTH: 848
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US-10-750-185-21192/c
; Sequence 21192, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
                                                                                                            Length
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 21192
LENGTH: 598
TYPE: DNA
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US-10-750-623-35778
; Sequence 35778, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
. APPLICANT: ROSENFELD, David
. APPLICANT: ROSENFELD, David
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US-10-750-623-35778
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| Similarity 85.7%;
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SEQ ID NO 35778
LENGTH: 848
TYPE: DNA
ORGANISM: BOVI
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APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
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Pred. No. 1.2e+02;
); Mismatches 2;
                                                                                                                                               Score 16.8; DB 7;
Pred. No. 1.2e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PatentIn version 3.3
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
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Sequence 35778, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
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US-11-112-908-46
    SEQ ID NOS:
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18; Conser
                                                                                                                                                                                                                                                                                                                                                  Sequence 46, Application Publication No. US20 GENERAL INFORMATION:
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APPLICANT: Davis,
                                                                          ; TYPE: DNA
; ORGANISM: Homo
US-11-112-908-44
                  SOFTWARE: Paten
SEQ ID NO 44
LENGTH: 150437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 46
1.ENGTH: 150491
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RESULT 10
US-10-750-185-27017

Sequence 27017, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:
APPLICANT: MI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, USPACHON
COMPOSITIONS FOR INFERRING BOVINE TRAITS
ITLE OF INVENTION: COMPOSITIONS FOR INFERRING
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
                 PatentIN version
NUMBER OF SEQ ID NOS:
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17; Conserv
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Best Local Similarity
Matches 17; Conser
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US-10-750-623-49007/c
                                                                   TYPE: DNA
CRGANISM: Bovine
US-10-750-185-49007
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US-10-750-623-49007
                                 SEQ ID NO 49007
LENGTH: 1077
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US-10-750-623-21192, Application US/10750623

Sequence 21192, Application US/10750623

Publication No. US20050287531A1

GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: KERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRA:

CURRENT APPLICATION NUMBER: US/10/750,623

CURRENT FILING DATE: 2003-12-31
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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                                                                                                                              Score 15.8; DB 6;
Pred. No. 2.4e+02;
L; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LOCATION: (1)...(64)
; OTHER INFORMATION: n is any nucleotide
US-10-750-623-21192
                                                                          any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-750-185-49007/c; Sequence 49007, Application US/10750185; Publication No. US20050260603A1; GENERAL INFORMATION:
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SOFTWARE: PatentIN version 3.1
EQ ID NO 21192
LENGTH: 598
                                                                                                                            th 68.7%;
Similarity 81.0%;
17; Conservative
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APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMBT01950
     MMBT01950
                                    , NAME/KEY: misc_feature
; LOCATION: (1)...(64)
; OTHER INFORMATION: n is
US-10-750-185-21192
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Best Local Similarity
Matches 17; Conser
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      Bovine
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APPLICANT:
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NAME/KEY:
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Publication No. US20050287531A1

GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: KERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRA

FILE REFERENCE: MMI1100-1

CURRENT APPLICATION NUMBER: US/10/750,623

CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1077;
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                          Score 15.8; DB 6; I Pred. No. 2.5e+02;
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Pred. No. 2.5e+02;
); Mismatches 2;
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 49007
LENGTH: 1077
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ilarity 89.5%;
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APPLICANT: KERR, KLULL.
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN' Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: 2002-12-31
PRIOR APPLICATION NUMBER: 2002-12-31
NUMBER OF SEQ ID NOS: 64992
SOFTWARE: PatentIN version 3.1
SEQ ID NO 40860
LENGTH: 1459
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US-10-750-185-63798/C
; Sequence 63798, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: RERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 63798
; LENGTH: 1836
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                                   Score 15.8; DB 6;
Pred. No. 2.6e+02;
); Mismatches 2,
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Pred. No. 2.6e+02;
0; Mismatches 2
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Publication No. US20050287531A1;
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
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US-10-750-623-48860
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 US-10-750-185-48860
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                                                                                           Length 1433;
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1.6e+02;
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Pred. No. 2.6e+02;
); Mismatches 2;
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Pred. No. 2.6e
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CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PatentIN version 3.1

SEQ ID NO 48860
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US-10-750-185-48860
Sequence 48860, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFE
                                                                                                                                                                                                                                                           RESULT 11
US-10-750-623-27017
; Sequence 27017, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: ROSENFELD, David
; APPLICANT: BATES, Stephen
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; LENGTH: 1433
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-27017
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; Publication No. US20050287531A1
; GENERAL INFORMATION:
    APPLICANT: MMI GENOMICS, INC.
    APPLICANT: MAI GENOMICS, INC.
    APPLICANT: ROSENFELD, David
    APPLICANT: ROSENFELD, David
    APPLICANT: HOLM, Tom
    APPLICANT: BATES, Stephen
    CURRENT APPLIANG BATE: 2003-12-31
    NUMBER OF SEQ ID NOS: 64922
    SOFTWARE: PATENTIN Version 3.1
    LENGTH: 1836
    TYPE: DNA
    ORGANISM: Bovine 19866880348213
US-10-750-623-63798
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l Similarity 89.5%;
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